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 SEQUENCE LENGTH (SQL): 2406
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 30 Jan 2004
 DEFINITION (DEF): Homo sapiens cDNA FLJ37276 fis, clone BRAMY2012426,
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 receptor ***Unc5H2*** mRNA.
 KEYWORDS (ST): oligo capping; fis (full insert sequence)
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

COMMENT:

NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.

REFERENCE:

1

AUTHOR (AU): Ota,T.; Suzuki,Y.; Nishikawa,T.; Otsuki,T.;
 Sugiyama,T.; Irie,R.; Wakamatsu,A.; Hayashi,K.;
 Sato,H.; Nagai,K.; Kimura,K.; Makita,H.; Sekine,M.;
 Obayashi,M.; Nishi,T.; Shibahara,T.; Tanaka,T.;
 Ishii,S.; Yamamoto,J.; Saito,K.; Kawai,Y.; Isono,Y.;
 Nakamura,Y.; Nagahari,K.; Murakami,K.; Yasuda,T.;
 Iwayanagi,T.; Wagatsuma,M.; Shiratori,A.; Sudo,H.;
 Hosoiri,T.; Kaku,Y.; Kodaira,H.; Kondo,H.; Sugawara,M.;
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 Kikkawa,E.; Omura,Y.; Abe,K.; Kamihara,K.; Katsuta,N.;
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 Togiya,S.; Komai,F.; Hara,R.; Takeuchi,K.; Arita,M.;
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 Aotsuka,S.; Yoshikawa,Y.; Matsunawa,H.; Ichihara,T.;
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 Takami,S.; Terashima,Y.; Suzuki,O.; Nakagawa,S.;
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 Tashiro,H.; Tanigami,A.; Fujiwara,T.; Ono,T.;
 Yamada,K.; Fujii,Y.; Ozaki,K.; Hirao,M.; Ohmori,Y.;
 Kawabata,A.; Hikiji,T.; Kobatake,N.; Inagaki,H.;
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 Matsumura,K.; Nakajima,Y.; Mizuno,T.; Morinaga,M.;
 Sasaki,M.; Togashi,T.; Oyama,M.; Hata,H.; Watanabe,M.;
 Komatsu,T.; Mizushima-Sugano,J.; Satoh,T.; Shirai,Y.;
 Takahashi,Y.; Nakagawa,K.; Okumura,K.; Nagase,T.;
 Nomura,N.; Kikuchi,H.; Masuho,Y.; Yamashita,R.;
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 Sugano,S.

TITLE (TI): Complete sequencing and characterization of 21,243
 full-length human cDNAs

OTHER SOURCE (OS): CA 140:158353
REFERENCE: 2
AUTHOR (AU): Tashiro,H.; Yamazaki,M.; Watanabe,K.; Kumagai,A.;
Itakura,S.; Fukuzumi,Y.; Fujimori,Y.; Komiyama,M.;
Sugiyama,T.; Irie,R.; Otsuki,T.; Sato,H.; Wakamatsu,A.;
Ishii,S.; Yamamoto,J.; Isono,Y.; Kawai-Hio,Y.;
Saito,K.; Nishikawa,T.; Kimura,K.; Yamashita,H.;
Matsuo,K.; Nakamura,Y.; Sekine,M.; Kikuchi,H.;
Kanda,K.; Wagatsuma,M.; Murakawa,K.; Kanehori,K.;
Takahashi-Fujii,A.; Oshima,A.; Sugiyama,A.;
Kawakami,B.; Suzuki,Y.; Sugano,S.; Nagahari,K.;
Masuho,Y.; Nagai,K.; Isogai,T.
TITLE (TI): NEDO human cDNA sequencing project
JOURNAL (SO): Unpublished
REFERENCE: 3 (bases 1 to 2406)
AUTHOR (AU): Isogai,T.; Yamamoto,J.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI
Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812,
Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975,
Fax:81-438-52-3986)

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L2 ANSWER 280 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

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SEQUENCE LENGTH (SQL): 276
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 3 Jul 2002
DEFINITION (DEF): Sequence 7 from Patent WO0233080.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 54 a 96 c 73 g 51 t 2 others
REFERENCE: 1
AUTHOR (AU): Koehler, R.H.
TITLE (TI): Regulation of human netrin binding membrane receptor
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JOURNAL (SO): Patent: WO 0233080-A 7 25-APR-2002; Bayer
Aktiengesellschaft (DE)

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LOCUS (LOC): AX451657 GenBank (R)
 GenBank ACC. NO. (GBN): AX451657
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 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 52 a 64 c 91 g 57 t
 REFERENCE: 1
 AUTHOR (AU): Koehler, R.H.
 TITLE (TI): Regulation of human netrin binding membrane receptor
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 JOURNAL (SO): Patent: WO 0233080-A 6 25-APR-2002; Bayer
 Aktiengesellschaft (DE)

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L2 ANSWER 282 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): AX451656 GenBank (R)
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 GenBank VERSION (VER): AX451656.1 GI:21698589
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 SEQUENCE LENGTH (SQL): 604
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 DIVISION CODE (CI): Patent
 DATE (DATE): 3 Jul 2002
 DEFINITION (DEF): Sequence 5 from Patent WO0233080.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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 Aktiengesellschaft (DE)

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601 cccg

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L2 ANSWER 283 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

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LOCUS (LOC):                AX451655      GenBank (R)
GenBank ACC. NO. (GBN):    AX451655
GenBank VERSION (VER):     AX451655.1  GI:21698588
CAS REGISTRY NO. (RN):     437596-46-8
SEQUENCE LENGTH (SQL):     313
MOLECULE TYPE (CI):        DNA; linear
DIVISION CODE (CI):        Patent
DATE (DATE):               3 Jul 2002
DEFINITION (DEF):          Sequence 4 from Patent WO0233080.
SOURCE:                     human.
  ORGANISM (ORGN):          Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                             Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                             Hominidae; Homo
NUCLEIC ACID COUNT (NA):   62 a    107 c    89 g    55 t
REFERENCE:                   1
  AUTHOR (AU):              Koehler,R.H.
  TITLE (TI):               Regulation of human netrin binding membrane receptor
                             ***unc5h*** -1
  JOURNAL (SO):             Patent: WO 0233080-A 4 25-APR-2002; Bayer
                             Aktiengesellschaft (DE)

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  181 tgagagctcc acttccctcc tggaggagga cgggacagcc ggacgttctc ctcgtgcccc
  241 tcggtgtccc gtgacagatc agcaaggaaa gggggtggga gtttggggag aaccagctct
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L2 ANSWER 284 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

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LOCUS (LOC):                AX451652      GenBank (R)
GenBank ACC. NO. (GBN):    AX451652
GenBank VERSION (VER):     AX451652.1  GI:21698587
CAS REGISTRY NO. (RN):     437596-45-7
SEQUENCE LENGTH (SQL):     2697
MOLECULE TYPE (CI):        DNA; linear
DIVISION CODE (CI):        Patent
DATE (DATE):               3 Jul 2002
DEFINITION (DEF):          Sequence 1 from Patent WO0233080.
SOURCE:                     human.
  ORGANISM (ORGN):          Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                             Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                             Hominidae; Homo
NUCLEIC ACID COUNT (NA):   503 a    906 c    807 g    481 t
REFERENCE:                   1
  AUTHOR (AU):              Koehler,R.H.
  TITLE (TI):               Regulation of human netrin binding membrane receptor

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FEATURES (FEAT):

Feature Key	Location	Qualifier
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L2 ANSWER 285 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC):

BM487397 GenBank (R)

GenBank ACC. NO. (GBN): BM487397

GenBank VERSION (VER): BM487397.1 GI:18608327

CAS REGISTRY NO. (RN): 397794-13-7

SEQUENCE LENGTH (SQL): 608

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 7 Feb 2002

DEFINITION (DEF): pgm2n.pk004.g9 Normalized Chicken Breast Muscle, Leg
Muscle, and Epiphyseal Growth Plate cDNA library

similar to ref|NP_071542.1 (NM_022206) transmembrane
receptor ***Unc5H1*** [Rattus norvegicus]
gb|AAB57678.1| (U87305) transmembrane receptor
UNC5H1 [Rattus norvegicus], mRNA sequence.
chicken.

SOURCE:

ORGANISM (ORGN):

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Archosauria; Aves; Neognathae;
Galliformes; Phasianidae; Phasianinae; Gallus

NUCLEIC ACID COUNT (NA): 107 a 214 c 195 g 91 t 1 others

COMMENT:

Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

REFERENCE:

1 (bases 1 to 608)

AUTHOR (AU): Cogburn, L.A.; Monsonego-Ornan, E.

TITLE (TI): ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library, USDA/IFAFA
Animal Genome Project

JOURNAL (SO): Unpublished (2002)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..608	/organism="Gallus gallus" /strain="Commercial broiler chickens and Ottawa Research Centre Strains 90 and 21" /db-xref="taxon:9031" /clone="pgm2n.pk004.g9" /clone-lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)" /sex="Male and Female" /tissue-type="Breast muscle, leg muscle and epiphyseal growth plate" /dev-stage="Breast, leg: Embryo (d19) ;post-hatch(1d,1,3,5,7,9,11 weeks);growth plate(1d,7d,14d post-hatch)" /lab-host="E. coli EMDH10B" /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

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601 ggcccgcc
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LOCUS (LOC): BC021657 GenBank (R)
 GenBank ACC. NO. (GBN): BC021657
 GenBank VERSION (VER): BC021657.1 GI:18203773
 CAS REGISTRY NO. (RN): 386533-01-3
 SEQUENCE LENGTH (SQL): 6420
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 3 Oct 2003
 DEFINITION (DEF): Mus musculus ankyrin 3, epithelial, mRNA (cDNA clone
 MGC:14049 IMAGE:4188590), complete cds.
 KEYWORDS (ST): MGC
 SOURCE: Mus musculus (house mouse)
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 1884 a 1623 c 1620 g 1293 t
 COMMENT:
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 18 Row: k Column: 4
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 25121951.
 REFERENCE: 1 (bases 1 to 6420)
 AUTHOR (AU): Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
 Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
 Shenmen, C.M.; Schuler, G.D.; Altschul, S.F.; Zeeberg, B.;
 Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
 Jordan, H.; Moore, T.; Max, S.I.; Wang, J.; Hsieh, F.;
 Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.;
 Hong, L.; Stapleton, M.; Soares, M.B.; Bonaldo, M.F.;
 Casavant, T.L.; Scheetz, T.E.; Brownstein, M.J.;
 Usdin, T.B.; Toshiyuki, S.; Carninci, P.; Prange, C.;
 Raha, S.S.; Loquellano, N.A.; Peters, G.J.; Abramson, R.D.;
 Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.; McKernan, K.J.;
 Malek, J.A.; Gunaratne, P.H.; Richards, S.; Worley, K.C.;
 Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
 Villalon, D.K.; Muzny, D.M.; Sodergren, E.J.; Lu, X.;
 Gibbs, R.A.; Fahey, J.; Helton, E.; Kettelman, M.; Madan, A.;
 Rodrigues, S.; Sanchez, A.; Whiting, M.; Madan, A.;
 Young, A.C.; Shevchenko, Y.; Bouffard, G.G.;
 Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
 Dickson, M.C.; Rodriguez, A.C.; Grimwood, J.; Schmutz, J.;
 Myers, R.M.; Butterfield, Y.S.; Krzywinski, M.I.;
 Skalska, U.; Smailus, D.E.; Schnerch, A.; Schein, J.E.;
 Jones, S.J.; Marra, M.A.
 TITLE (TI): Generation and initial analysis of more than 15,000
 full-length human and mouse cDNA sequences
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
 (2002)
 OTHER SOURCE (OS): CA 138:67676
 REFERENCE: 2 (bases 1 to 6420)
 AUTHOR (AU): Strausberg, R.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (14-JAN-2002) National Institutes of Health,
 Mammalian Gene Collection (MGC), Cancer Genomics
 Office, National Cancer Institute, 31 Center Drive,

FEATURES (FEAT):

Feature Key	Location	Qualifier
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gene	1..6420	/gene="Ank3" /note="synonym: MGC14049" /db-xref="LocusID:11735" /db-xref="MGI:88026"
CDS	385..5565	/codon-start=1 /product="Ank3 protein" /protein-id="AAH21657.1" /db-xref="GI:18203774" /db-xref="LocusID:11735" /translation="MSEEPKEKPAKPAHRKRKGK KSDANASYLRAARAGHLEKALDYI KNGVDVNICNQNGLNALHLASKEGHVEVVSELLQ REANVDAATKKGNTALHIASLAGQ AEVVKVLVTNGANVNAQSQNGFTPLYMAAQENHL EVRVRLDNGASQSLATEDGFTPL AVALQQGHDQVVSLLLENDTKGKVRLPALHIAAR KDDTKAAALLQNDTNADVESKSG FTPLHIAAHYGNINVATLLLNRAAAVDFTARNDI TPLHVASKRGNANMVKLLLDRGAK IDAKTRDGLTPLHCGARSQHEQVVEMLLDRSAPI LSKTKNGLSPLHMAATQGDHLNCVQ LLLQHNVPVDDVTNDYLTALHVAAHCGHYKVAKV LLDKKASPNAKALNGFTPLHIACK KNRIRVMELLLKHGASIQAVTESGLTPIHVAAFM GHVNIIVSQLMHHGASPNTTNVRGE TALHMAARSGQAEVVRYLVQDGAQVEAKAKDDQT PLHISARLGKADIVQQLLQQGASP NAATTSGYTPLHLAAREGHEDVAAFLLDHGASLS ITTKKGFTPLHVAARYGKLEVASL LLQKSASPDAAGKSGLTPLHVAAHYDNQKVALLL LDQGASPHAAAKNGYTPLHIAAKK NQMDIATSLLEYGADANAVTRQGIASVHLAAQEG HVDMSVSLLLSRNANVNLSNKSGLT PLHLAAQEDRVNVAEVLVNQGAHVDAQTKMGYTP PHVGCHYGNIKIVNFLQHSKVN AKTKNGYTALHQAAQQGHTHIINVLLQNNASPNE LTVNGNTALAIARRLGYSVVDTL KVVTEEIMTTTTITEKHKNVPETMNEVLDMSSD EGEDAITGDTDKYLGPDLDKELGD DSLPAEGYVGFSLGARSASLRSFSSDRSYTLNRS SYARDSMMIEELLVPSKEQHLTFT REFDSDSLRHYSWAADTLDNVNLVSSPVHSGFLV SFMVDARGGSMRGSRRHGMRIIP PRKCTAPTRITCRLVKRHLNPPPMVEGEGLAS RLVEMGPAGAQFLGPVIVEIPHFG SMRGKERELIVLRSENGETWKEHQFDSKNEDLAE LLNGMDEELDSPPELGTKRICRII TKDFPQYFAVVSRIKQESNQIGPEGGILSSTTV LVQASFPEGALTKRIRVGLQAQPV PEETVKKILGNKATFSPIVTVPRRRKFHKPITM TIPVPPPSGEGVSNGYKGDATPNL RLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFT TNVSARFWLADCHQVLETVGLASQ LYRELICVPYMAKFVVFATNDPVESSLRCFCMT

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misc-feature 3214..3528

misc-feature 4672..4953

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Alpha-helical domain present in a
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these domains form homotypic and
heterotypic dimers"
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SOURCE: Homo sapiens adult brain cDNA to mRNA, clone:fh19201.
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AUTHOR (AU): Nakajima,D.; Nakayama,M.; Nagase,T.; Ohara,O.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (25-JAN-2001) Daisuke Nakajima, Kazusa DNA Research Institute, Laboratory for Genome Informatics; Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:nakajima@kazusa.or.jp, Tel:81438523915, Fax:81438523914)

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6121	atgtactccc	acaaaaat	tattggcctt	tttgtaagag	atgaaaaaga	attgacacag
6181	ttctctttta	agagaagaac	ttttttatta	ttattttttat	ctccaactgc	aggtgggtgc
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6301	tcactaaaac	agggttctct	ttggattaaa	agttctggat	ttattgcaac	tattttctct
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6421	ggttttagat	aatatcttct	actgccaaac	ttctggcaaa	tttacctgtg	aatttcaaaa
6481	tgttataaaa	tctcttgata	tgcttttgtt	tttcctttta	gccattttct	cttcaatttc
6541	ttagtccctc	tgccctctgt	aaatgtgttg	agtgatatag	ctatcagatg	tattgaaggc
6601	aaagttctcg	cagaggtctc	tgttccagct	ctgtaaagg	cacaggaatc	gtgaaggagc
6661	tgagaaatct	tctctctcgg	cccactgtct	gtggcccat	gtcattgttt	cctcatgaaa
6721	cattgcagag	tttgaatcct	cagtaactct	cattgactgg	attagaggtg	atggccacag
6781	caaattggag	agcaaaatgt	tggcctacag	agaattgacac	aattttatct	gcctttgggtg
6841	ttagttggcca	tagtgctgta	tttgaaaatc	gatgcttttag	ccaaaagctg	aatgaccacc
6901	gtttccgtag	tttccactgt	tttgtctgca	tagaattttc	ctgaactaca	agcaaaaatg
6961	tattttgtcc	aatgtcacaa	aagtga	gttactaatc	tt	

GenBank ACC. NO. (GBN): BM271771
 GenBank VERSION (VER): BM271771.1 GI:17965045
 CAS REGISTRY NO. (RN): 387745-80-4
 SEQUENCE LENGTH (SQL): 577
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 20 Dec 2001
 DEFINITION (DEF): ig38h09.x1 HR85 islet Homo sapiens cDNA 3' similar to
 TR:O08721 O08721 TRANSMEMBRANE RECEPTOR ***UNC5H1***
 . ; , mRNA sequence.

SOURCE:
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 117 a 194 c 165 g 101 t

COMMENT:

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave., Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 475.

REFERENCE: 1 (bases 1 to 577)
 AUTHOR (AU): Melton,D.; Brown,J.; Kenty,G.; Permutt,A.; Lee,C.;
 Kaestner,K.; Lemishka,I.; Searce,M.; Brestelli,J.;
 Gradwohl,G.; Clifton,S.; Hillier,L.; Marra,M.; Pape,D.;
 Wylie,T.; Martin,J.; Blistain,A.; Schmitt,A.;
 Theising,B.; Ritter,E.; Ronko,I.; Bennett,J.;
 Cardenas,M. ; Gibbons,M.; McCann,R.; Cole,R.;
 Tsagareishvili,R.; Williams,T., Jackson,Y. ; Bowers,Y.
 TITLE (TI): Endocrine Pancreas Consortium
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..577	/organism="Homo sapiens" /db-xref="taxon:9606" /clone-lib="HR85 islet" /tissue-type="Purified pancreatic islet" /lab-host="DH10B" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site-1: NotI; Site-2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692

SEQUENCE (SEQ):

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1  ggccggccgcc acacactgca ccacagctct cccacctctg aggccgagga gttcgtctcc
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121  gggaccttca acttcctcgg gggccggctg atgatcccta atacaggtag gaaggacccc
181  agggggctct gagagctcca cttccctcct ggaggaggac gggacagccg gacgttcctc
241  tcgtgcccct cgggtgtccc tgacagatca gcaaggaaag ggggtggagt tttggggaga
301  acccagtctt ggctggcacc gagggcgtgg ccagagctgt cttcctcttg ttgcctgtgg
361  gcacaaggta attgtccatt catttacaca gccaaagcag ctacttggtc cagtctccat
421  gtggggccct gggcccagag gtagggcaag ccccgggccc aaggagcttg caactgagca
481  gggagacaac caagggcaaa cagatgagca cgggcctggg cagaggccat cctggagtcc
541  cactgcatc ctggcttcca cccaccccag caccgaa

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L2 ANSWER 289 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): BI900830 GenBank (R)
 GenBank ACC. NO. (GBN): BI900830
 GenBank VERSION (VER): BI900830.1 GI:16188624
 CAS REGISTRY NO. (RN): 363722-14-9
 SEQUENCE LENGTH (SQL): 548
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 24 Sep 2003
 DEFINITION (DEF): ib81g04.y4 Amplified Melton Mouse Islets 1 MIS1-A Mus
 musculus cDNA clone IMAGE:5653063 5' similar to
 TR:O08721 O08721 TRANSMEMBRANE RECEPTOR ***UNC5H1***
 . ; , mRNA sequence.

KEYWORDS (ST): EST
 SOURCE: Mus musculus (house mouse)
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 104 a 195 c 150 g 99 t

COMMENT:

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu)
 MGI:1939389 This sequence now available from the IMAGE consortium,
 for clone orders contact: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 441.

REFERENCE: 1 (bases 1 to 548)
 AUTHOR (AU): Melton,D.; Meadows,A.; Clifton,S.; Hillier,L.;
 Marra,M.; Pape,D.; Wylie,T.; Martin,J.; Blistain,A.;
 Schmitt,A.; Theising,B.; Ritter,E.; Ronko,I.;
 Bennett,J.; Cardenas,M.; Gibbons,M.; McCann,R.;
 Cole,R.; Tsagareishvili,R.; Williams,T.; Jackson,Y.;
 Bowers,Y.
 TITLE (TI): WashU-Harvard Pancreas EST Project
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..548	/organism="Mus musculus" /mol-type="mRNA" /strain="ICR" /db-xref="taxon:10090" /clone="IMAGE:5653063"

/tissue-type="Islets of
 Langerhans"
 /dev-stage="Adult"
 /lab-host="DH10B"
 /clone-lib="Amplified Melton Mouse
 Islets 1 MIS1-A"
 /note="Organ: Pancreas; Vector:
 pSPORT1; Site-1: Not 1; Site-2:
 Sal 1; Library constructed using
 SuperScript Plasmid Library kit
 (Life Technologies). cDNA made by
 oligo-dT priming. Size-selected by
 column fractionation; average
 insert size 0.91 kb. Amplified
 once on solid support. cDNA
 Library Preparation: Guolin Chen.
 "

SEQUENCE (SEQ):

```

1  tacatcacac  gggagcacag  cctagtcgtg  cggcaggccc  gcctggccga  cactgccaac
61  tacacctgcg  tggccaagaa  catcgtggcc  cgctcgccgaa  gcgcctctgc  ggccgtcatt
121  gtatatgtgg  atgggagctg  gagcccatgg  agtaagtgg  cagcctgctgc  gcttgactgc
181  acccactggc  ggagccggga  ttgttccgac  ccagcgcccc  gcaacggagg  tgaggagtgc
241  cggggtgctg  acctggacac  ccgcaactgt  accagtgacc  tctgcctgca  cacctcttcc
301  ggccccgagg  acgtggctct  ctacatcgcc  ctgcctgccc  tggccgtgtg  cctcatcttg
361  ctgctgctgg  tcctcgctct  catctactgc  cgcaagaagg  aaggactgga  ctgagacgtg
421  gctgactcat  ccataccttac  ctcaggcttc  cagcctgtca  gcatcaagcc  cagcaaagca
481  gacaatcccc  atctgctcac  catccaaccg  gacctcagca  ccaccacgac  cacctaccag
541  ggcagcct
  
```

L2 ANSWER 290 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): BC009333 GenBank (R)
 GenBank ACC. NO. (GBN): BC009333
 GenBank VERSION (VER): BC009333.2 GI:40226527
 CAS REGISTRY NO. (RN): 342081-81-6
 SEQUENCE LENGTH (SQL): 2688
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 1 Feb 2005
 DEFINITION (DEF): Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA
 clone IMAGE:4126760), partial cds.
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

COMMENT:

On Dec 19, 2003 this sequence version replaced gi:14424611.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found

Series: IRAL Plate: 26 Row: g Column: 22.

Differences found between this sequence and the human genome (build 35) are described in misc_difference features below.

REFERENCE: 1 (bases 1 to 2688)
AUTHOR (AU): Strausberg,R.L.; Feingold,E.A.; Grouse,L.H.;
Derge,J.G.; Klausner,R.D.; Collins,F.S.; Wagner,L.;
Shenmen,C.M.; Schuler,G.D.; Altschul,S.F.; Zeeberg,B.;
Buetow,K.H.; Schaefer,C.F.; Bhat,N.K.; Hopkins,R.F.;
Jordan,H.; Moore,T.; Max,S.I.; Wang,J.; Hsieh,F.;
Diatchenko,L.; Marusina,K.; Farmer,A.A.; Rubin,G.M.;
Hong,L.; Stapleton,M.; Soares,M.B.; Bonaldo,M.F.;
Casavant,T.L.; Scheetz,T.E.; Brownstein,M.J.;
Usdin,T.B.; Toshiyuki,S.; Carninci,P.; Prange,C.;
Raha,S.S.; Loquellano,N.A.; Peters,G.J.; Abramson,R.D.;
Mullahy,S.J.; Bosak,S.A.; McEwan,P.J.; McKernan,K.J.;
Malek,J.A.; Gunaratne,P.H.; Richards,S.; Worley,K.C.;
Hale,S.; Garcia,A.M.; Gay,L.J.; Hulyk,S.W.;
Villalon,D.K.; Muzny,D.M.; Sodergren,E.J.; Lu,X.;
Gibbs,R.A.; Fahey,J.; Helton,E.; Kettelman,M.; Madan,A.;
Rodrigues,S.; Sanchez,A.; Whiting,M.; Madan,A.;
Young,A.C.; Shevchenko,Y.; Bouffard,G.G.;
Blakesley,R.W.; Touchman,J.W.; Green,E.D.;
Dickson,M.C.; Rodriguez,A.C.; Grimwood,J.; Schmutz,J.;
Myers,R.M.; Butterfield,Y.S.; Krzywinski,M.I.;
Skalska,U.; Smailus,D.E.; Schnerch,A.; Schein,J.E.;
Jones,S.J.; Marra,M.A.
TITLE (TI): Generation and initial analysis of more than 15,000
full-length human and mouse cDNA sequences
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
(2002)
OTHER SOURCE (OS): CA 138:67676
REFERENCE: 2 (bases 1 to 2688)
AUTHOR (AU): Director MGC Project.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (12-JUN-2001) National Institutes of Health,
Mammalian Gene Collection (MGC), Cancer Genomics
Office, National Cancer Institute, 31 Center Drive,
Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2688	/organism="Homo sapiens" /mol-type="mRNA" /db-xref="taxon:9606" /clone="IMAGE:4126760" /tissue-type="Brain, neuroblastoma" /clone-lib="NIH-MGC-19" /lab-host="DH10B-R" /note="Vector: pOTB7"
gene	<1..2688	/gene="UNC5A" /note="synonyms: UNC5H1, KIAA1976" /db-xref="LocusID:90249" /db-xref="MIM:607869"
CDS	<1..1627	/gene="UNC5A" /codon-start=2 /product="UNC5A protein" /protein-id="AAH09333.2" /db-xref="GI:40226528" /db-xref="LocusID:90249" /db-xref="MIM:607869" /translation="DVALYVGLIAVAVCLVLLLL VLILVYCRKKEGLDSDVADSSILT SGFQPVSIKPSKADNPHELLTIQPDLTSTTTTYYQG SLCPRQDGPSPKFQLTNGHLLSPL GGGRHTLHHSSPTSEAEFEVSRLSTQNYFRSLPR GTSNMTYGTFFNFLGGRLMIPNTGI

misc-difference 2244

misc-difference 2636..2688

SEQUENCE (SEQ):

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1381 gaagataatt tccagcctgg acccaccctg taggcggggt gccgactggc ggactctggc
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1681 caggcagaag ccggacaggg gcccttcccc acaccgggga gagctgctcg gacaggcccc
1741 ctcccgccg aagctgtccc ttaatgtctg tccttcagac cctgcccgaag ctcccacctc
1801 tccatggcct gcctagccag gctggcactg ccactcacac tccggccccg ggcccaggag
1861 ggacagtgcc tggagcctgg gccaggccca gccatctgtg gtgtgtgtat gtgctgtga
1921 tgctacctct cctcccgctc ctctccaggg gccccgcata cacacggcca tgcacgcaca
1981 cactgggctt gggccagggc cccagagctc ctgcctgagc tggaccttat gcaaacattt
2041 ctgtgcctgc tgggtagggg cacgtctgag gggccctgct ccaagcctgc aggaccgagg
2101 gccacagccg gacagggggt agcccttgga ttcaggcaca cgaccaccac acgagcacgt
2161 gccacgcatg cctcgtgtgc tcatctcaca cacaccccc tcccgggtca cgcagacacc
2221 ccccaaccac acacatctca tgccgtacac ctgaggctgc tcacgtctca cggccagtgt
2281 tgggtcacat ttgcctctca catgctgccc tctccacca cccagggaca ccccacggct
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GenBank ACC. NO. (GBN): BG938104
 GenBank VERSION (VER): BG938104.1 GI:14337476
 CAS REGISTRY NO. (RN): 340854-24-2
 SEQUENCE LENGTH (SQL): 460
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 11 Jun 2001
 DEFINITION (DEF): lAbo11D02 Bovine Abomasum cDNA Library Bos taurus cDNA
 5', mRNA sequence.
 SOURCE: Cow.
 ORGANISM (ORGN): Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Cetartiodactyla;
 Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos
 NUCLEIC ACID COUNT (NA): 129 a 84 c 123 g 124 t
 COMMENT:

Contact: Dr. Stephen Moore
 . Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: smooore@afns.ualberta.ca
 The sequence best matches gb:HS34B21 (Human DNA sequence from clone
 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a
 novel protein with ZU5 domain similar to part of Tight Junction
 Protein ZO1 (TJP1) and ***UNC5*** Homologs, the gene for a novel BZR
 alue
 of 1e-40
 PCR Primers
 FORWARD: M13 Forward
 BACKWARD: M13 Reverse
 Seq primer: T3 primer
 High quality sequence stop: 460.

REFERENCE: 1 (bases 1 to 460)
 AUTHOR (AU): Moore,S.S.; Hansen,C.; Li,C.; Fu,A.; Meng,Y.; Li,G.
 TITLE (TI): cDNA's from bovine abomasum tissue
 JOURNAL (SO): Unpublished (2001)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..460	/organism="Bos taurus" /db-xref="taxon:9913" /clone-lib="Bovine Abomasum cDNA Library" /sex="Two males and one female mixed" /tissue-type="Gastrointestinal tissue (GIT)" /cell-type="Epithelial" /dev-stage="Young adult" /lab-host="XL1-BlueMRF'-strain" /note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site-1: EcoR I; Site-2: Xho I"

SEQUENCE (SEQ):

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121 ccgacctttc catgccaagg atcggatgtg gtcttgatcg tctgcaatgg gaaaatgtat
181 ccgcaataat tgaggaggtc tttgaggcaa cacagatcag aattactgtg tacacactct
241 gaacagaaga gcatttttgga tgtgtctacc ttctgcatca cctggggccac aggactgagc
301 aaactgacct taaaatggtc agaggaccgt ttcttgtgaa gtagtctgtg ttacaggcca
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421 taggaatttt tctttttcag gaaggtaagg ggaggggacca
  
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LOCUS (LOC): AK018177 GenBank (R)
 GenBank ACC. NO. (GBN): AK018177
 GenBank VERSION (VER): AK018177.1 GI:12857775
 CAS REGISTRY NO. (RN): 322347-06-8
 SEQUENCE LENGTH (SQL): 3866
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): High-Throughput CDNA Sequencing
 DATE (DATE): 3 Apr 2004
 DEFINITION (DEF): Mus musculus adult male medulla oblongata cDNA, RIKEN
 full-length enriched library, clone:6330415E02
 product:TRANSMEMBRANE RECEPTOR ***UNC5H2*** homolog
 [Rattus norvegicus], full insert sequence.
 KEYWORDS (ST): HTC; CAP trapper
 SOURCE: Mus musculus (house mouse)
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 COMMENT:
 Please visit our web site (<http://genome.gsc.riken.jp/>) for further
 details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to Rot = 10.0 and subtraction to
 Rot = 100.0. Second strand cDNA was prepared with the primer
 adapter of sequence [5'
 GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
 with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
 bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
 end: BamHI. Host: DH10B.
 REFERENCE: 1
 AUTHOR (AU): Carninci,P.; Hayashizaki,Y.
 TITLE (TI): High-efficiency full-length cDNA cloning
 JOURNAL (SO): Meth. Enzymol., 303, 19-44 (1999)
 OTHER SOURCE (OS): CA 131:318304
 REFERENCE: 2
 AUTHOR (AU): Carninci,P.; Shibata,Y.; Hayatsu,N.; Sugahara,Y.;
 Shibata,K.; Itoh,M.; Konno,H.; Okazaki,Y.;
 Muramatsu,M.; Hayashizaki,Y.
 TITLE (TI): Normalization and subtraction of cap-trapper-selected
 cDNAs to prepare full-length cDNA libraries for rapid
 discovery of new genes
 JOURNAL (SO): Genome Res., 10 (10), 1617-1630 (2000)
 OTHER SOURCE (OS): CA 134:305920
 REFERENCE: 3
 AUTHOR (AU): Shibata,K.; Itoh,M.; Aizawa,K.; Nagaoka,S.; Sasaki,N.;
 Carninci,P.; Konno,H.; Akiyama,J.; Nishi,K.;
 Kitsunai,T.; Tashiro,H.; Itoh,M.; Sumi,N.; Ishii,Y.;
 Nakamura,S.; Hazama,M.; Nishine,T.; Harada,A.;
 Yamamoto,R.; Matsumoto,H.; Sakaguchi,S.; Ikegami,T.;
 Kashiwagi,K.; Fujiwake,S.; Inoue,K.; Togawa,Y.;
 Izawa,M.; Ohara,E.; Watahiki,M.; Yoneda,Y.;
 Ishikawa,T.; Ozawa,K.; Tanaka,T.; Matsuura,S.;
 Kawai,J.; Okazaki,Y.; Muramatsu,M.; Inoue,Y.; Kira,A.;
 Hayashizaki,Y.
 TITLE (TI): RIKEN integrated sequence analysis (RISA)
 system--384-format sequencing pipeline with 384
 multicapillary sequencer
 JOURNAL (SO): Genome Res., 10 (11), 1757-1771 (2000)
 OTHER SOURCE (OS): CA 134:203311
 REFERENCE: 4
 AUTHOR (AU): The RIKEN Genome Exploration Research Group Phase II

TITLE (TI): Functional annotation of a full-length mouse cDNA collection
 JOURNAL (SO): Nature, 409, 685-690 (2001)
 OTHER SOURCE (OS): CA 134:203311
 REFERENCE: 5
 AUTHOR (AU): The FANTOM Consortium; the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE (TI): Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL (SO): Nature, 420, 563-573 (2002)
 OTHER SOURCE (OS): CA 138:131939
 REFERENCE: 6 (bases 1 to 3866)
 AUTHOR (AU): Adachi,J.; Aizawa,K.; Akahira,S.; Akimura,T.; Arai,A.; Aono,H.; Arakawa,T.; Bono,H.; Carninci,P.; Fukuda,S.; Fukunishi,Y.; Furuno,M.; Hanagaki,T.; Hara,A.; Hayatsu,N.; Hiramoto,K.; Hiraoka,T.; Hori,F.; Imotani,K.; Ishii,Y.; Itoh,M.; Izawa,M.; Kasukawa,T.; Kato,H.; Kawai,J.; Kojima,Y.; Konno,H.; Kouda,M.; Koya,S.; Kurihara,C.; Matsuyama,T.; Miyazaki,A.; Nishi,K.; Nomura,K.; Numazaki,R.; Ohno,M.; Okazaki,Y.; Okido,T.; Owa,C.; Saito,H.; Saito,R.; Sakai,C.; Sakai,K.; Sano,H.; Sasaki,D.; Shibata,K.; Shibata,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Suzuki,H.; Tagami,M.; Tagawa,A.; Takahashi,F.; Tanaka,T.; Tejima,Y.; Toya,T.; Yamamura,T.; Yasunishi,A.; Yoshida,K.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..3866	/organism="Mus musculus" /mol-type="mRNA" /strain="C57BL/6J" /db-xref="FANTOM-DB:6330415E02" /db-xref="taxon:10090" /clone="6330415E02" /sex="male" /tissue-type="medulla oblongata" /clone-lib="RIKEN full-length enriched mouse cDNA library" /dev-stage="adult"
CDS	417..3254	/note="unnamed protein product; TRANSMEMBRANE RECEPTOR UNC5H2 homolog [Rattus norvegicus] (SPTR O08722, evidence: FASTY, 96.5%ID, 100%length, match=2835) putative" /codon-start=1 /protein-id="BAB31108.1" /db-xref="GI:12857776" /translation="MRARSGVRSALLLALLLCWD PTPSLAGVDSAGQVLPDSYPSAPA EQLPYFLLLEPQDAYIVKNKPVELHLCRAFPATQIY FKCNGEWSVQNDHVTQESLDEATG LRVREVQIEVSRQQVEELFGLEDYWCQCVAWSSS GTTKSRRAYIRIAYLRKNFDQEPL AKEVPLDHEVLLQCRPPEGVPVAEVEWLKNEDVI DPAQDTNFLTIDHNLIIRQARLS DTANYTCVAKNIVAKRRSTAATVIVYVNGGWSSW

APLNGGAFCEGQAFQKTACTTVCPVDGAWTEWSK
 WSACSTECAHWSRECMAPPQNG
 GRDCSGTLLDSKNCTDGLCVLNQRTLNDPKSHPL
 ETSGDVALYAGLVVAVFVVAVLM
 AEGVIVYRRNCRDFDITDSSAALTGGFHPVNF
 KTARPNNPQLLHPSAPDLTASAG
 IYRGPVYALQDSADKIPMTNSPLLDPLPSLKIKV
 YNSSTIGSGSLADGADLLGVLP
 GTYPGDFSRDTHFLHLRSASLGSQHLLGLPRDPS
 SSVSGTFGCLGGRLSLPGTGVSL
 VPNGAIPQGFYDLYLHINKAESTLPLSEGSQTV
 LSPSVTCGPTGLLLCRPVVLTVP
 CAEVIAGDWIFQLKTOAHQGHWEVVTLDDEETLN
 TPCYCQLEAKSCHILLDQLGSYVF
 MGESYSRSAVKRLQLAIFAPALCTSLEYSRLRVYC
 LEDTPVALKEVLELERTLGGYLVE
 EPKPLLFKDSYHNRLSLHDIPHAWRSKLLAKY
 QEIPFYHVWNGSQRALHCTFTLER
 HSLASTEFTCKVCVRQVEGEGQIFQLHTTLAETP
 AGSLDALCSAPGNAITTQLGPYAF
 KIPLSIRQKICSSLDAPDSRGNDWRLLAQKLSMD
 RYLNYPATKASPTGVILDLWEARQ
 QDDGDLNSLASALEEMGKSEMLVAMATDGDC"

SEQUENCE (SEQ) :

1	attgtggccg	gcggcagggc	gggcgagggc	gcggagccgc	ggggagcggc	agggcgcaga
61	gggaagcaca	cacccactc	ggacagactt	gcgcgcgcgc	ccgctacgag	cgccgctgag
121	cgactccac	tgggatcgca	caacttcgga	gcaggcgcg	gacggcgctc	gcagcgggag
181	agcgcgaaa	gggcgcacca	gagccgggat	ccccagcggc	gtccgactcc	cggagcgctc
241	ctagtcgccg	ggcggcctcc	cggcgctgcg	cggttgcttc	tgcgcttacg	gagggcacgg
301	gctggcgctg	ccgggcgcct	gcgagaacgg	cgaggcggcg	gcgaaggcga	aggcggcgag
361	gctggggacc	gggaaagaac	cccaggggag	aggcgcccgg	gccgggggac	aggagcatga
421	gggcccggag	cggggtgcgg	agcgcgctgc	tgctggcgct	gctgctttgc	tgggatccga
481	caccgagcct	agcaggcggt	gactctgctg	gccagggtgct	cccagactcc	tacccatcag
541	cccctgcgga	gcagctgccg	tacttcctat	tggagccaca	ggacgcctac	atcgtaaaga
601	acaagccagt	ggaactgcac	tgcagagcct	tccctgccac	gcagatctac	ttcaagtgtg
661	atggcgagtg	ggtcagccag	aatgaccacg	tcacacagga	gagcctggat	gaggccacag
721	gcttgccggg	gcgagaggtg	cagatcgagg	tgctacggca	gcaagtggag	gaactcttcg
781	ggctcgagga	ctactggtgc	cagtgcgtgg	cctggagctc	ttcggaact	accaagagtc
841	gccgagccta	catccgcatt	gcctacttgc	gcaagaactt	tgaccaggag	cctctggcca
901	aggaggtacc	cttggatcat	gaggtccttc	tgcaagtgcg	cccaccggag	ggagtgcctg
961	tggctgaggt	ggaatggctc	aagaatgaag	atgtcattga	ccccgctcag	gacactaact
1021	tcctgctcac	cattgaccac	aacctcatca	tcgcgccaggc	gcgcctctca	gacacggcca
1081	actacacctg	tgtggccaag	aatatcgtgg	ccaagcgccg	gagcaccgcg	gccacagtca
1141	tcgtctatgt	gaatggaggc	tgggtccagct	gggcagagtg	gtcaccctgt	tccaatcgct
1201	gtggccgagg	ctggcagaag	cgtactcgga	cctgcaccaa	tccagcccca	ctcaatggag
1261	gcgccttctg	tgagggacag	gccttccaga	agacagcttg	caccaccgtg	tgcccagtgg
1321	atggagcgtg	gaccgagtgg	agcaagtggg	ctgcctgcag	cacagagtgt	gcgcactggc
1381	gcagccgcga	gtgcatggca	ccgccacccc	agaagcgagg	ccgtgactgc	agcgggacgc
1441	tacttgactc	caagaactgc	actgatgggc	tgctcgctgc	gaatcacaga	actctaaacg
1501	accctaaaag	ccacccccctg	gagacatcgg	gagatgtggc	actgtacgca	ggccttggtg
1561	tggccgtctt	tgtggtggta	gcggttctca	tggccgaggg	agtgatcgta	taccggagaa
1621	actgccggga	cttcgacacg	gacatcaccc	actcctctgc	ggccctcact	ggtggcttcc
1681	accctgtcaa	cttcaagact	gcaaggccca	acaaccgcga	gctcctgcac	ccgtccgccc
1741	ctccagacct	aacggccagt	gctggcatct	accgcggggc	tgtgtatgcc	ctgcaggact
1801	ccgccgacaa	gatccccatg	actaatcgc	ccctgctgga	tcccctgccc	agcctcaaga
1861	tcaaggtcta	taactccagc	accatcggtt	ctgggtctgg	cctggctgat	ggagccgacc
1921	tgctgggtgt	cctcccgcgc	ggcacgtacc	caggcgattt	ctcccgggac	accatttcc
1981	tgcacctgcg	cagtgccagc	cttgggtccc	agcacctcct	gggcctacct	cgggacccca
2041	gcagcagtg	cagcggcacc	tttgggtgcc	tgggaggaag	gctgagcctc	cccggcacag
2101	gggtcagcct	gttggtagca	aatggagcca	ttccccaggg	caagtcttat	gacctgtatc
2161	tacatatcaa	caaggccgaa	agcaccctcc	cactttcaga	aggttcccag	acagtattga
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2461	tcatgggcga	gtcctactct	cgctctgcag	tcaagcggct	ccagctggcc	atcttcgccc
2521	cagccctctg	cacctccctg	gagtatagcc	tcagggtcta	ctgtctggag	gacacacctg

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2641 ccaagcctttt gctcttttaag gacagttacc acaacctacg cctctccctc catgacatcc
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2761 tctggaatgg cagccagaga gccctgcact gcactttcac cctggagagg catagcctgg
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3781 cccagttttt tagggaacgc aaatgattta ttatccagat acttggatag ttccttttta
3841 agaaaacaaa acaaacaaaa aaaagt

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L2 ANSWER 293 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): BG147430 GenBank (R)
 GenBank ACC. NO. (GBN): BG147430
 GenBank VERSION (VER): BG147430.1 GI:12650838
 CAS REGISTRY NO. (RN): 320542-32-3
 SEQUENCE LENGTH (SQL): 428
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Feb 2001
 DEFINITION (DEF): mac03h05.y1 Soares mouse 3NbMS Mus musculus cDNA clone
 IMAGE:3998840 5' similar to TR:O08722 O08722
 TRANSMEMBRANE RECEPTOR ***UNC5H2*** . ;, mRNA
 sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 90 a 145 c 108 g 84 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1496568
 Seq primer: -40RP from Gibco
 High quality sequence stop: 332.

REFERENCE: 1 (bases 1 to 428)
 AUTHOR (AU): NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..428	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="IMAGE:3998840" /clone-lib="Soares mouse 3NbMS" /sex="male" /tissue-type="Spleen" /dev-stage="4 weeks" /lab-host="DH10B"

(Pharmacia) with a modified
polylinker; Site-1: Not I; Site-2:
Eco RI; 1st strand cDNA was primed
with a Not I - oligo(dT) primer
[5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGT
TTTTTTTTTTTTTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia),
digested with Not I and cloned
into the Not I and Eco RI sites of
the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan.
Library went through three rounds
of normalization, and was
constructed by Bento Soares and
M.Fatima Bonaldo."

SEQUENCE (SEQ):

```

1 agcctttgct ctttaaggac agttaccaca acctacgcct ctccctccat gacatcccc
61 atgcccactg gaggagcaaa ctactggcca agtaccagga gattcccttc taccacgtct
121 ggaatggcag ccagagagcc ctgcactgca ctttcaccct ggagaggcat agcctggcct
181 ccacggagtt cacctgtaag gtctgcgtgc ggcaggtcga aggggaaggc cagattttcc
241 agctgcacac aacgttggcc gagacgcctg ctggctccct ggatgctctc tgctctgccc
301 cgggcaatgc catcaccacc canctgggac cctatgcctt caagataccc ctgtgcattc
361 gcccaaagat atttggaag cctgggacgc cccaactcc cggggcaacg actggaggct
421 gttggcgc

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L2 ANSWER 294 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): BG016570 GenBank (R)
GenBank ACC. NO. (GBN): BG016570
GenBank VERSION (VER): BG016570.1 GI:12469947
CAS REGISTRY NO. (RN): 318165-78-5
SEQUENCE LENGTH (SQL): 675
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 19 Feb 2003
DEFINITION (DEF): df62c02.x1 Xenopus laevis unfertilized egg cDNA library
Xenopus laevis cDNA clone IMAGE:3743978 3' similar to
TR:O08722 O08722 TRANSMEMBRANE RECEPTOR ***UNC5H2***
. ;, mRNA sequence.
KEYWORDS (ST): EST
SOURCE: Xenopus laevis (African clawed frog)
ORGANISM (ORGN): Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Amphibia; Batrachia; Anura;
Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus

NUCLEIC ACID COUNT (NA): 227 a 129 c 115 g 204 t

COMMENT:

Other ESTs: df62c02.y1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Source lab clone id - xlneg004e03 This clone is available
royalty-free through LLNL; contact the IMAGE Consortium
(image@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 471.

REFERENCE: 1 (bases 1 to 675)

AUTHOR (AU): Clifton, S.; Johnson, S.L.; Blumberg, B.; Song, J.;

Underwood, K.; Theising, B.; Bowers, Y.; Person, B.M;
 Gibbons, M.; Harvey, N.; Ritter, E.; Jackson, Y.;
 McCann, R.; Waterston, R.; Wilson, R.
 WashU Xenopus EST project, 1999
 Unpublished (1999)

TITLE (TI):
 JOURNAL (SO):

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..675	/organism="Xenopus laevis" /db-xref="taxon:8355" /clone="IMAGE:3743978" /clone-lib="Xenopus laevis unfertilized egg cDNA library" /tissue-type="unfertilized egg" /lab-host="Top-10 F" /note="Vector: pBluescript SK-; Site-1: EcoRI; Site-2: XhoI; This library has been used successfully to clone a number of full-length cDNAs ranging in size from 1.4 to 4.5 kb. There are less than 0.5% clones with multiple inserts. Since each cDNA has an EcoRI site at its 5' end and an XhoI site at the 3' end, these clones can be easily identified. One should be suspicious of any clone which gives 3 or more bands in an EcoRI-XhoI double digest AND has an internal XhoI site. We usually do not further characterize any such clones unless the cDNA is known to give multiple bands in an EcoRI-XhoI digest. Microplate status: 500,000 unamplified cDNAs were mass excised (pBluescript SK-) in X11-Blue using ExAssist phage. The resulting single-stranded phagemids were used to infect Top10F'. Clones were picked into freezing medium (per liter 15 g tryptone, 10g yeast extract, 5g NaCl, 36 mM K2HPO4, 13.2 mM KH2PO4, 1.7 mM Na-citrate, 0.4 mM MgSO4*7 H2O, 6.8 mM (NH4)2SO4, 4% w/v glycerol) and grown for 24 hours. Original library construction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XGC) library"

SEQUENCE (SEQ):

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1 ttttttttttc aaattttgtc atttaatat taaaaaaaaa gattcatcca cagatctgga
61 taataaataa tgctgcattt cctaaaaaaaa ccatttgcca tatcagttag gctgttccaa
121 atctggatac gataaaatca gttggttttg ggtaatcaga taccaatgat gatagaaaaa
181 gagaataaaa agagaaaata taacattatg tagtattaaa agcgtagcat gttaagggtg
241 aacacatctg ccagcagtta ccatgatgcc agtaattcct ttttcgtatg caagtaatga
301 gggcataaat atattccagt agacacttga atggcttgta aacagagttt ttaagaattt
361 ctaaggctgg ttgcgattgg actttaagga gaatgtccat cccatctcct tactaaagt
421 tagttctgga gttatcatca taatcaagga ccacaactgt ctcttggttaa tggccagagg
481 acatcctcca ccaacctact ttgtctttca gagattcacc aactcatatc aactgagtaa
541 cgaagtcatt agcaatcccc atcggttgcc attacaagca tcatctcgct tttaccatt
601 tcctccaagg caactagcaa gagtggtgaa gtcaccatca atctggagta aggcttctca

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LOCUS (LOC): BF723349 GenBank (R)
GenBank ACC. NO. (GBN): BF723349
GenBank VERSION (VER): BF723349.1 GI:12024426
CAS REGISTRY NO. (RN): 313039-24-6
SEQUENCE LENGTH (SQL): 413
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 3 Jan 2001
DEFINITION (DEF): mab31f11.y1 Soares NMEBA branchial arch Mus musculus
cDNA clone IMAGE:3971877 5' similar to TR:008721 O08721
TRANSMEMBRANE RECEPTOR ***UNC5H1*** . ; , mRNA
sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 99 a 119 c 112 g 83 t

COMMENT:
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1471909
Seq primer: -40RP from Gibco
High quality sequence stop: 408.

REFERENCE: 1 (bases 1 to 413)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..413	/organism="Mus musculus" /db-xref="taxon:10090" /clone="IMAGE:3971877" /clone-lib="Soares-NMEBA-branchial-arch" /tissue-type="branchial arches" /dev-stage="embryo, 10.5 dpc" /lab-host="DH10B (phage resistant)" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: NotI; Site-2: EcoRI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATGCA TTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

SEQUENCE (SEQ):

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1  cgtccctcga gtacaacatc cgagtgtact gcctgcacga caccacgat gctctcaagg
61 aggtggtgca gctggagaag cagctgggtg gacagctgat ccaggagccc cgtgtcctgc
121 acttcaaaga cagttaccac aacctacgtc tgtccatcca cgacgtgccc agctccctgt
181 ggaagagcaa gctccttgct agctaccagg agatcccttt ttaccacatc tggaatggca
241 ctccagcagta tctgcactgc accttcaccc tggagcgcgt caatgccagc accagcgacc
301 tggcctgcaa ggtgtgggtg tggcaggtgg agggagatgg acagagcttc aacatcaact
361 ttaacatcac taaggacacg aggtttgctg aaatgctggc tctggagagt gaa

```

L2 ANSWER 296 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): BF149887 GenBank (R)
 GenBank ACC. NO. (GBN): BF149887
 GenBank VERSION (VER): BF149887.1 GI:11031282
 CAS REGISTRY NO. (RN): 300498-28-6
 SEQUENCE LENGTH (SQL): 379
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 29 Dec 2000
 DEFINITION (DEF): uy79c08.y1 NCI CGAP Mam5 Mus musculus cDNA clone
 IMAGE:3665774 5' similar to TR:008722 008722
 TRANSMEMBRANE RECEPTOR ***UNC5H2*** . ; , mRNA
 sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 78 a 136 c 94 g 70 t 1 others
 COMMENT:

Other ESTs: uy79c08.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1426542

Seq primer: -40RP from Gibco

High quality sequence stop: 321.

REFERENCE: 1 (bases 1 to 379)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..379	/organism="Mus musculus" /strain="C57/B6" /db-xref="taxon:10090" /clone="IMAGE:3665774" /clone-lib="NCI-CGAP-Mam5" /tissue-type="tumor, gross tissue" /dev-stage="7 months" /lab-host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

SEQUENCE (SEQ):

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1 caacctacgc ctctccctcc atgacatccc ccatgcccac tggaggagca aactactggc
61 caagtaccag gagattccct tctaccacgt ctggaatggc agccagagag ccctgcactg
121 cactttcacc ctggagaggg atagcctggc ctccacggag ttcacctgta aggtctgcgt
181 gcggcaggtc gaaggggaag gccagatttt ccagctgcac acaacgttgg ccgagacgcc
241 tgctggctcc ctggatgctc tctgctctgc cccgggcaat gccatcacca cccagctggg
301 accctatgcc ttcaagatac ccctgtccat ccgccanaag atctgcagca gcctggacgc
361 ccccaacttt ccgggggac
```

L2 ANSWER 297 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): BF011550 GenBank (R)
GenBank ACC. NO. (GBN): BF011550
GenBank VERSION (VER): BF011550.1 GI:10711825
CAS REGISTRY NO. (RN): 296511-01-8
SEQUENCE LENGTH (SQL): 425
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 6 Oct 2000
DEFINITION (DEF): us40e11.y1 Soares NMEBA branchial arch Mus musculus
cDNA clone IMAGE:3169580 5' similar to TR:008722 O08722
TRANSMEMBRANE RECEPTOR ***UNC5H2*** . ; , mRNA
sequence.

SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 88 a 149 c 110 g 77 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1065040
Seq primer: -40RP from Gibco
High quality sequence stop: 385.

REFERENCE: 1 (bases 1 to 425)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..425	/organism="Mus musculus" /db-xref="taxon:10090" /clone="IMAGE:3169580" /clone-lib="Soares-NMEBA-branchial-arch" /tissue-type="branchial arches" /dev-stage="embryo, 10.5 dpc" /lab-host="DH10B (phage resistant)" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: NotI; Site-2: EcoRI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATGCA TTTTTTTTTTTTTTTTTTTTTTTT 3']";

to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned
 into the Not I and Eco RI sites of
 the modified pT7T3 vector.
 Library constructed and normalized
 by Bento Soares and M.Fatima
 Bonaldo."

SEQUENCE (SEQ):

```

1 gttaccacaa cctacgcctc tccctccatg acatccccca tgcccactgg aggagcaaac
61 tactggccaa gtaccaggag attcccttct accacgtctg gaatggcagc cagagagccc
121 tgcactgcac ttccaccctg gagaggcata gcctggcctc cacggagttc acctgtaagg
181 tctgcgtgcg gcaggtcgaa ggggaaggcc agattttcca gctgcacaca acgttggcgg
241 agacgcctgc tggctccctg gatgctctct gctctgcccc gggcaatgcc atcaccaccc
301 agctgggacc ctatgccttc aagatacccc tgtccatccg ccaaaagatc tgcagcagcc
361 tggacgcccc caactcccgg ggcaacgact ggaggctgtt ggcgcanaag ctgtccatgg
421 gccgg

```

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LOCUS (LOC): AK022859 GenBank (R)
 GenBank ACC. NO. (GBN): AK022859
 GenBank VERSION (VER): AK022859.1 GI:10434495
 CAS REGISTRY NO. (RN): 390321-80-9
 SEQUENCE LENGTH (SQL): 1948
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 30 Jan 2004
 DEFINITION (DEF): Homo sapiens cDNA FLJ12797 fis, clone NT2RP2002066,
 highly similar to Rattus norvegicus transmembrane
 receptor ***Unc5H2*** mRNA.
 KEYWORDS (ST): oligo capping; fis (full insert sequence)
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

COMMENT:

NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing and clone selection:
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.

REFERENCE:

1
 AUTHOR (AU): Ota, T.; Suzuki, Y.; Nishikawa, T.; Otsuki, T.;
 Sugiyama, T.; Irie, R.; Wakamatsu, A.; Hayashi, K.;
 Sato, H.; Nagai, K.; Kimura, K.; Makita, H.; Sekine, M.;
 Obayashi, M.; Nishi, T.; Shibahara, T.; Tanaka, T.;
 Ishii, S.; Yamamoto, J.; Saito, K.; Kawai, Y.; Isono, Y.;
 Nakamura, Y.; Nagahari, K.; Murakami, K.; Yasuda, T.;
 Iwayanagi, T.; Wagatsuma, M.; Shiratori, A.; Sudo, H.;
 Hosoiri, T.; Kaku, Y.; Kodaira, H.; Kondo, H.; Sugawara, M.;
 Takahashi, M.; Kanda, K.; Yokoi, T.; Furuya, T.;
 Kikkawa, E.; Omura, Y.; Abe, K.; Kamihara, K.; Katsuta, N.;
 Sato, K.; Tanikawa, M.; Yamazaki, M.; Ninomiya, K.;
 Ishibashi, T.; Yamashita, H.; Murakawa, K.; Fujimori, K.;
 Tanai, H.; Kimata, M.; Watanabe, M.; Hiraoka, S.; Chiba, Y.;
 Ishida, S.; Ono, Y.; Takiguchi, S.; Watanabe, S.;
 Yosida, M.; Hotuta, T.; Kusano, J.; Kanehori, K.;
 Takahashi-Fujii, A.; Hara, H.; Tanase, T.; Nomura, Y.;
 Togiya, S.; Komai, F.; Hara, R.; Takeuchi, K.; Arita, M.;
 Imose, N.; Musashino, K.; Yuuki, H.; Oshima, A.; Sasaki, N.;
 Aotsuka, S.; Yoshikawa, Y.; Matsunawa, H.; Ichihara, T.;
 Shiohata, N.; Sano, S.; Moriya, S.; Momiyama, H.; Satoh, N.;
 Takami, S.; Terashima, Y.; Suzuki, O.; Nakagawa, S.;
 Senoh, A.; Mizoguchi, H.; Goto, Y.; Shimizu, F.; Wakebe, H.;

Kawakami,B.; Yamazaki,M.; Watanabe,K.; Kumagai,A.;
 Itakura,S.; Fukuzumi,Y.; Fujimori,Y.; Komiyama,M.;
 Tashiro,H.; Tanigami,A.; Fujiwara,T.; Ono,T.;
 Yamada,K.; Fujii,Y.; Ozaki,K.; Hirao,M.; Ohmori,Y.;
 Kawabata,A.; Hikiji,T.; Kobatake,N.; Inagaki,H.;
 Ikema,Y.; Okamoto,S.; Okitani,R.; Kawakami,T.;
 Noguchi,S.; Itoh,T.; Shigeta,K.; Senba,T.;
 Matsumura,K.; Nakajima,Y.; Mizuno,T.; Morinaga,M.;
 Sasaki,M.; Togashi,T.; Oyama,M.; Hata,H.; Watanabe,M.;
 Komatsu,T.; Mizushima-Sugano,J.; Satoh,T.; Shirai,Y.;
 Takahashi,Y.; Nakagawa,K.; Okumura,K.; Nagase,T.;
 Nomura,N.; Kikuchi,H.; Masuho,Y.; Yamashita,R.;
 Nakai,K.; Yada,T.; Nakamura,Y.; Ohara,O.; Isogai,T.;
 Sugano,S.

TITLE (TI): Complete sequencing and characterization of 21,243
 full-length human cDNAs
 JOURNAL (SO): Nat. Genet., 36 (1), 40-45 (2004)
 OTHER SOURCE (OS): CA 140:158353
 REFERENCE: 2
 AUTHOR (AU): Isogai,T.; Ota,T.; Hayashi,K.; Sugiyama,T.; Otsuki,T.;
 Suzuki,Y.; Nishikawa,T.; Nagai,K.; Sugano,S.;
 Aotsuka,S.; Yoshikawa,Y.; Matsunawa,H.; Ishii,S.;
 Kawai,Y.; Saito,K.; Yamamoto,J.; Wakamatsu,A.;
 Nakamura,Y.; Nagahari,K.; Masuho,Y.; Sasaki,N.
 TITLE (TI): NEDO human cDNA sequencing project
 JOURNAL (SO): Unpublished
 REFERENCE: 3 (bases 1 to 1948)
 AUTHOR (AU): Isogai,T.; Otsuki,T.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (23-AUG-2000) Takao Isogai, Helix Research
 Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
 Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
 Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1948	/organism="Homo sapiens" /mol-type="mRNA" /db-xref="taxon:9606" /clone="NT2RP2002066" /cell-line="NT2" /cell-type="teratocarcinoma" /clone-lib="NT2RP2" /note="cloning vector: pME18SFL3~mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction
CDS	204..1304	/note="unnamed protein product" /codon-start=1 /protein-id="BAB14276.1" /db-xref="GI:10434496" /translation="MYLLINKAESTLPLSEGTQT VLSPSVTCGPTGLLLCRPVILTMP HCAEVSARDWIFQLKTOAHQGHWEVVTLDEETL NTPCYCQLEPRACHILLDQLGTYV FTGESYSRSAVKRLQLAVFAPALCTSLEYSRLRVY CLEDTPVALKEVLELERTLGGYLV EEPKPLMFKDSYHNRLSLHDLPHAHWSKLLAK YQEIPFYHIWSGSQKALHCTFTLE RHSLASTELTCKICVRQVEGEGQIFQLHTTLAET PAGSLDTLCSAPGSTVTTQPGPYA FKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSM DRYLNYPATKASPTGVILDLWEAL QQDDGDLNSLASALEEMGKSEMLVAVATDGDC"

SEQUENCE (SEQ):

1 ctacgcattt cgcccgggac acccacttcc tgcacctgcg cagcgccagc ctcggttccc

```

121 tgggtgggag gctcagcatc cccggcacag ggggtcagctt gctgggtgcc aatggagcca
181 ttccccaggg caagtcttac gagatgtatc tactcatcaa caaggcagaa agtaccctcc
241 cgctttcaga agggacccag acagtattga gcccctcggt gacctgtgga cccacaggcc
301 tcctgctgtg ccgccccgtc atcctcacca tgccccactg tgccgaagtc agtgcccggtg
361 actggatctt tcagctcaag acccaggccc accagggccca ctgggaggag gtggtgaccc
421 tggatgagga gacctgaac acaccctgct actgccagct ggagcccagg gcctgtcaca
481 tcctgctgga ccagctgggc acctacgtgt tcacgggcga gtcctattcc cgctcagcag
541 tcaagcggct ccagctggcc gtcttcgccc ccgcccctctg cacctccctg gagtacagcc
601 tccgggtcta ctgcctggag gacacgcctg tagcactgaa ggaggtgctg gagctggagc
661 ggactctggg cggatacttg gtggaggagc cgaaaccgct aatgttcaag gacagttacc
721 acaacctgcy cctctccctc catgacctcc cccatgccca ttggaggagc aagctgctgg
781 ccaaatacca ggagatcccc ttctatcaca tttggagtgg cagccagaag gccctccact
841 gcactttcac cctggagagg cacagcttgg cctccacaga gctcacctgc aagatctgcy
901 tgcggcaagt ggaaggggag ggccagatat tccagtgca taccactctg gcagagacac
961 ctgctggctc cctggacact ctctgctctg cccctggcag cactgtcacc acccagccgg
1021 gaccttatgc cttcaagatc ccactgtcca tccgccagaa gatatgcaac agcctagatg
1081 cccccaactc acggggcaat gactggcgga tgttagcaca gaagctctct atggaccggt
1141 acctgaatta ctttgccacc aaagcgagcc ccacgggtgt gatcctggac ctctgggaag
1201 ctctgcagca ggacgatggg gacctcaaca gcctggcgag tgcttggag gagatgggca
1261 agagtगत gctggtggct gtggccaccg acggggactg ctgagcctcc tgggacagcy
1321 ggctggcagg gactggcagg aggcaggtgc agggaggcct ggggcagcct cctgatgggg
1381 atgtttggcc tctgcttctc cccagttcac agccagagtt gcctctcctc ctctcttcc
1441 ccaaccccca gaccatgacc agccttagaa aatccatgta ctctgttgtt agagggccca
1501 gagttccttc tccacccccg ctctctctct cttggcctga gatctctgtg caggaacca
1561 gatggggctg aagcctctgg aggcagtgtg ttgggggcgg gcaggcagga ggccctccct
1621 ccacccccc accctcagcc cggcaacttc ttgggttccat gggttttagt tccgttctcg
1681 ttttcttctc cgtttattga tttctccttt ctccctaagc ccccttctgc ttccacgccc
1741 ttttctctct tgaagagtca agtacaattc agacaaactg ctttctcctg tccaaaagca
1801 aaaaggcaaa ggaaagaaaag aaagcttcag accgctagta aggtctaaaag aagaagaaaa
1861 acaccaaacc cacaagggaa aagaaaaacc cagtttctta ggaaacgcaa acgatttatt
1921 atccagatta tttggataag tccttttt

```

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```

LOCUS (LOC): AL359832 GenBank (R)
GenBank ACC. NO. (GBN): AL359832
GenBank VERSION (VER): AL359832.33 GI:18121472
CAS REGISTRY NO. (RN): 274663-97-7
SEQUENCE LENGTH (SQL): 195130
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 9 Feb 2005
DEFINITION (DEF): Human DNA sequence from clone RP11-790G19 on chromosome
10 Contains the 5' end of the gene for transmembrane
receptor ***Unc5H2*** ( ***UNC5H2*** ), the 3' end
of a novel gene and two CpG islands, complete sequence.
KEYWORDS (ST): HTG; ***UNC5H2***
SOURCE: Homo sapiens (human)
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

```

COMMENT:

On Jan 10, 2002 this sequence version replaced gi:18072481.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>
RP11-790G19 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6
----- Genome Center

Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

REFERENCE: 1 (bases 1 to 195130)
AUTHOR (AU): Howden, P.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (04-FEB-2005) Wellcome Trust Sanger
Institute, Hinxton, Cambridgeshire, CB10 1SA, UK.
E-mail enquiries: vega@sanger.ac.uk Clone requests:
clonerequest@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..195130	/organism="Homo sapiens" /mol-type="genomic DNA" /db-xref="taxon:9606" /chromosome="10" /clone="RP11-790G19" /clone-lib="RPCI-11.3"
misc-feature	2000	/note="Clone-right-end: RP11-814L17"
misc-feature	10028..10092	/note="Single clone region. Assembly confirmed by restriction digest data."
misc-feature	10145..10214	/note="Single clone region. Assembly confirmed by restriction digest data."
gene	join(189651..190145, AL359384.17:63772..6399 6, AL359384.17:68671..6881 4, AL359384.17:69277..6938 0, AL359384.17:70640..7082 0, AL359384.17:71549..7171 6, AL359384.17:72519..7268 3, AL359384.17:72909..7294 1, AL359384.17:74866..7506 0, AL359384.17:75383..7577 2, AL359384.17:76418..7650 5, AL359384.17:77356..7752 4, AL359384.17:77651..7788 4, AL359384.17:79762..7991 1, AL359384.17:80529..8069 3, AL359384.17:81860..8204 1, AL359384.17:83063..8681	/gene="UNC5B"

mRNA

```
join(189651..190145,  
AL359384.17:63772..6399  
6,  
AL359384.17:68671..6881  
4,  
AL359384.17:69277..6938  
0,  
AL359384.17:70640..7082  
0,  
AL359384.17:71549..7171  
6,  
AL359384.17:72519..7268  
3,  
AL359384.17:72909..7294  
1,  
AL359384.17:74866..7506  
0,  
AL359384.17:75383..7577  
2,  
AL359384.17:76418..7650  
5,  
AL359384.17:77356..7752  
4,  
AL359384.17:77651..7788  
4,  
AL359384.17:79762..7991  
1,  
AL359384.17:80529..8069  
3,  
AL359384.17:81860..8204  
1,  
AL359384.17:83063..8681  
5)
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/locus-tag="RP11-5801.1-002"  
/gene="UNC5B"
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gene

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join(190008..190145,  
AL359384.17:63772..6399  
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AL359384.17:68671..6881  
4,  
AL359384.17:69277..6938  
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AL359384.17:70640..7082  
0,  
AL359384.17:71549..7171  
6,  
AL359384.17:72519..7268  
3,  
AL359384.17:74866..7506  
0,  
AL359384.17:75383..7577  
2,  
AL359384.17:76418..7650  
5,  
AL359384.17:77356..7752  
4,  
AL359384.17:77651..7788  
4,  
AL359384.17:79762..7991  
1,  
AL359384.17:80529..8069  
3,  
AL359384.17:81860..8204  
1,  
AL359384.17:83063..8681
```

```
/locus-tag="RP11-5801.1-002"  
/product="unc-5 homolog B (C.  
elegans) "  
/note="match: cDNAs: AK018177.1"  
/gene="UNC5B"
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mRNA

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join(190008..190145,  
AL359384.17:63772..6399  
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AL359384.17:68671..6881  
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AL359384.17:69277..6938  
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AL359384.17:70640..7082  
0,  
AL359384.17:71549..7171  
6,  
AL359384.17:72519..7268  
3,  
AL359384.17:74866..7506  
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2,  
AL359384.17:76418..7650  
5,  
AL359384.17:77356..7752  
4,  
AL359384.17:77651..7788  
4,  
AL359384.17:79762..7991  
1,  
AL359384.17:80529..8069  
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AL359384.17:81860..8204  
1,  
AL359384.17:83063..8681  
5)
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/gene="UNC5B"  
  
/locus-tag="RP11-58O1.1-001"  
/product="unc-5 homolog B (C.  
elegans)"  
/note="match: ESTs: AI144009.1  
AI344433.1 AI962233.1 BQ182589.1  
BU500256.1 match: cDNAs:  
AL049370.1 AY126437.1"  
/gene="UNC5B"
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CDS

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join(190067..190145,  
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6,  
AL359384.17:68671..6881  
4,  
AL359384.17:69277..6938  
0,  
AL359384.17:70640..7082  
0,  
AL359384.17:71549..7171  
6,  
AL359384.17:72519..7268  
3,  
AL359384.17:74866..7506  
0,  
AL359384.17:75383..7577  
2,  
AL359384.17:76418..7650  
5,  
AL359384.17:77356..7752  
4,  
AL359384.17:77651..7788  
4,  
AL359384.17:79762..7991  
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L2 ANSWER 300 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

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LOCUS (LOC): AL359384 GenBank (R)
GenBank ACC. NO. (GBN): AL359384
GenBank VERSION (VER): AL359384.17 GI:15620618
CAS REGISTRY NO. (RN): 272420-55-0
SEQUENCE LENGTH (SQL): 122288
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 9 Feb 2005
DEFINITION (DEF): Human DNA sequence from clone RP11-5801 on chromosome
10 Contains the 5' end of a novel gene, the gene for
transmembrane receptor ***Unc5H2*** ( ***UNC5H2***
), the 5' end of the gene for equilibrative nucleoside
transporter 3 (ENT3) and a CpG island, complete
sequence.
KEYWORDS (ST): HTG; ENT3; ***UNC5H2***
SOURCE: Homo sapiens (human)
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

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COMMENT:

On Sep 14, 2001 this sequence version replaced gi:15131810.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>
RP11-5801 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>

 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

REFERENCE: 1 (bases 1 to 122288)
 AUTHOR (AU): Brown, A.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (04-FEB-2005) Wellcome Trust Sanger
 Institute, Hinxton, Cambridgeshire, CB10 1SA, UK.
 E-mail enquiries: vega@sanger.ac.uk Clone requests:
 clonerequest@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
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misc-feature 120289

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120001	gtaccacaaa	ctgggtagct	gaaaagcaag	gctctaggga	ataacatttc	cttgctgctg
120061	ctttggcatt	ttttggctca	tggcagcatc	actgcagtct	gtggctctgt	cttcacgcag
120121	cctctgcctg	tgtgtctgtg	tgtccttccc	tcttttcccg	tatactgtgg	attgaggggt
120181	cattcctcct	ccagtaggat	ctcctcttaa	ctaagcatgt	ctgcaaagac	cctatgtcca
120241	gataagtcac	atcctgaggt	tctgggtaga	catgaatttt	gggggcatga	attcagcccc
120301	ctctagacgg	ggtagcatgc	agtgtctgga	ttgtgaggaa	caagaccagg	ccttgggttac
120361	aggtgggctg	cgaggaggac	gctgaggacc	cttagaggaa	atgtttcccc	agggcagccg
120421	ggagggacac	ggctttggca	gtggcaacat	ggactacatt	ttcaaggagt	gtggagtga
120481	ggggaggagg	ggcctggttc	ctggaggcag	caaagttaaa	gtagtttttt	tttctttacc
120541	caaagggaga	cctaagagag	tctcttggcc	agcagagaaa	ggaacaagca	gcagtgaggg
120601	aaagagaaaa	tgcaggcaag	aaaggtggga	ttcatgggtg	gagtcctcag	gaagtcaagt
120661	taggctggag	gaagagccct	ttttgcggag	tggaaaggag	gtgtgctcca	gaaagccttg
120721	cacacactgc	aaggaggaag	gcggggaagc	tcattccaga	agacaggaa	tttgctcatc
120781	gtccagcagg	gattcctgag	gaggtgtgag	aaaggattga	aggctgggga	gagccccggg
120841	gtgctcagag	agcaagattt	acagtgagcc	caggcctgga	gctgtcatga	gaggccaaag
120901	gagggacggt	tgcatgcaag	ggtcagatgg	ggaccctctt	ccttaggggtg	gccacagtgg
120961	cttcgtctgt	ctggccagca	ttttccagag	cttacctgtc	tgattctgac	cccagatttg
121021	tccttccctt	gggcctctgg	cctccccttc	agcctggctg	catctagcct	cctgcctggc
121081	ccctggaaca	ggcattgccc	cccttccctg	cccagccagc	cctcccagct	ggtccctgcc
121141	cttggccaca	caccatttat	ctttcctgag	ccagtgtctc	aaacacaggg	ccttgggaact
121201	tgacagaaag	ttaccagccc	cacccttat	ggggacatct	gccctctgct	cacctcattt
121261	tgctcaggaa	tgatctgggc	tgatgccag	ggcaagggca	cctcccctgc	aatatcccag
121321	gcgcagaaac	tcagctatcc	gaaagcgcca	agtttgcaat	ggcaaacctat	tcttggctcc
121381	aacctgctcg	ctgctgctaa	tttcatgccc	ctgtgatcca	ggtaacgctc	tgctgccttg
121441	agctgccacc	cccaggcttg	aatcgctttt	cctcgcccgc	ccggtaggag	cccagctgcc
121501	tctgctgctg	cttctctggag	gtgggggctg	cacaaagctg	cctcgcagaa	gccactcagc
121561	agcacggaca	ctgagtctgc	cgcagctcgt	gactaatttg	ctgcacttat	ttcaaagtgc
121621	ccaaatggca	ttcagggaag	agaaagctta	accagggtct	gccagagata	aacgggctca
121681	tttcgggggc	tccctgcccc	aagaaacctc	tttacctgga	ctctgagcct	ggaattgaat
121741	tcttccagaa	gagaccctta	gcacggagcc	tctcagtgtg	gcggaggaga	ggaaatgtgg
121801	cccgctcataa	aatgggcctc	acatctggcc	agctggctct	gggtgggctt	taaattgtgt
121861	ttgaagagca	tctctccctt	ttcctgggtg	tcgcaaactg	ggtcagtgtg	gcaaattggaa
121921	atgagtttcc	ttctcaccat	agcgagcaac	tcaagtgcc	ccctgcccag	gccagcagtg
121981	gctcatccac	attcaccac	catatggggg	taccctggcg	cctggcacc	ctgggccagg
122041	gcctgtccac	agcttgggtg	aggaaccccc	atgccacccc	tgggccagtc	tgggtgaggc
122101	ccccatgccc	actctggggc	tctttgcagg	ggttgacag	taaggcgaga	gcttgggaagc
122161	ctgccccatg	ctgccccccc	acagacactc	tttaacatgg	tctttgctta	gctgccaaacc
122221	atgtccgtca	attttgggta	actgacagag	gtgggggctt	ttctcttaat	ctttttcttt
122281	tcttttct					

GenBank ACC. NO. (GBN): AF129475
 GenBank VERSION (VER): AF129475.1 GI:6002701
 CAS REGISTRY NO. (RN): 243886-90-0
 SEQUENCE LENGTH (SQL): 600
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Other vertebrates
 DATE (DATE): 1 Oct 1999
 DEFINITION (DEF): Petromyzon marinus netrin receptor ***UNC5*** (***UNC5***) mRNA, partial cds.
 SOURCE: sea lamprey.
 ORGANISM (ORGN): Petromyzon marinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzontiformes; Petromyzontidae; Petromyzon
 NUCLEIC ACID COUNT (NA): 156 a 150 c 171 g 123 t
 REFERENCE: 1 (bases 1 to 600)
 AUTHOR (AU): Shifman,M.I.; Selzer,M.E.
 TITLE (TI): Expression of the netrin receptor UNC-5 selectively in poorly regenerating neurons following spinal transection in lamprey
 JOURNAL (SO): Neurorehabil. Neural Repair (1999) In press
 REFERENCE: 2 (bases 1 to 600)
 AUTHOR (AU): Shifman,M.I.; Selzer,M.E.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (18-FEB-1999) Neurology, University of Pennsylvania, 452 Stemmler Hall, 36th Street and Hamilton Walk, Philadelphia, PA 19104, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..600	/organism="Petromyzon marinus" /db-xref="taxon:7757" /tissue-type="brain"
gene	<1..>600	/gene="UNC5"
CDS	<1..>600	/gene="UNC5" /codon-start=3 /product="netrin receptor UNC5" /protein-id="AAF00103.1" /db-xref="GI:6002702" /translation="HREEQARYIVKNKPVTMSCA ASPATQIYFKCNGEWLHQKAHHIE EREDETTGRSVREVQTDVSRQQVEELFGLLEDYWC QCVAWSAAGTSKSRKAYVRLAYLR KNFEQKPLGKYALLDHEVLLHCRPPDAIPQAEVE WLKSEEIIDPVIDQNFYITVDHNL IIKQTRLADSANYTCVAKNLVAKRRSSTATITVY VNGGW"

SEQUENCE (SEQ):

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      1 tacatcgtga agaacaagcc cgttacatcg tgaagaataa gccggtcacc atgagctgcg
     61 ccgcctcgcc cgccaccag atctacttca agtgcaacgg ggagtggctc caccagaagg
    121 cccatcacat tgaggagagg gaggatgaga caacagggcg gtcagtacgg gaggttcaga
    181 cagacgtgtc tcggcagcag gtggaggagc tgtttgggct ggaggactac tgggtgtcaat
    241 gcgtcgccctg gagtgcagcc ggcaccagca agagccgcaa ggcttatgtc cgcttagcat
    301 atttgcgga gaattttgag caaaagccat tgggcaaata tgctcttctt gaccatgaag
    361 ttctgttgca ttgtcgccct cctgatgccca ttccccaagc cgaggtggag tggttgaaaa
    421 gtgaagaaat tattgacca gtcataagtc aaaacttcta catcacggta gatcacaacc
    481 taataattaa gcagactcgg ctggcagaca gtgctaacta cacgtgcgtt gccagaatc
    541 tgggtggccaa gcggcggagc tctactgccca cgatcaccgt gtatgtcaac ggcggctgga
  
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L2 ANSWER 302 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): AI951556 GenBank (R)
 GenBank ACC. NO. (GBN): AI951556
 GenBank VERSION (VER): AI951556.1 GI:5743866
 CAS REGISTRY NO. (RN): 242027-40-3
 SEQUENCE LENGTH (SQL): 788

DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 9 Mar 2000
 DEFINITION (DEF): wv36f04.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone
 IMAGE:2531647 3' similar to TR:008721 008721
 TRANSMEMBRANE RECEPTOR ***UNC5H1*** . ;, mRNA
 sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 154 a 266 c 210 g 154 t 4 others
 COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
 Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1125 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 446.

REFERENCE: 1 (bases 1 to 788)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..788	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2531647" /clone-lib="NCI-CGAP-Ov18" /tissue-type="fibrotheoma" /lab-host="DH10B (phage-resistant)" /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCAGC ATTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```

1  ccgaggagtt cgtctccgc ctctccgcc agaactactt ccgctccctg ccccgaggca
61  ccagcaacat gacctatggg accttcaact tcctcggggg ccggctgatg atccctaata
121 caggaatcag cctcctcatc cccccagatg ccataccccg agggaagatc tatgagatct
181 acctcacgct gcacaagccg gaagacgtga ggttgccctt agctggctgt cagaccctgc
241 tgagtcccat cgttagctgt ggaccccttg gcgttctgct caccgggcca gtcactctgg
301 ctatggacca ctgtggggag cccagccctg acagctggag cctgcgcctc aaaaagcagt
361 cgtgcgaggg cagctgggag gatgtgctgc acctgggcga ggaggcgccc tcccacctct

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481 ccctgggtggg agaggccctc agcgtggctg ccgccaaagcg cctcaagctg cttctgtttg
541 cgccggtggc ctgcacctcc ctgcagtaca acatactggt ctactgcctg catgacactc
601 acgatgcact caacgtagtg gtgcagctgg agaagcagct gcagggacag ctgatccagg
661 agccactggg actgcacttc aaggacagtt accacaacct gcgcctatnc atccacgatg
721 tgcccagctn ccntgtggag agtaagcttc ttgtcagcta cccagagatc cncatatatca
781 catcctgg

L2 ANSWER 303 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): AI508226 GenBank (R)
GenBank ACC. NO. (GBN): AI508226
GenBank VERSION (VER): AI508226.1 GI:4407131
CAS REGISTRY NO. (RN): 228275-13-6
SEQUENCE LENGTH (SQL): 517
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 15 Mar 2000
DEFINITION (DEF): mh5lg07.y1 Soares mouse placenta 4NbMP13.5 14.5 Mus
musculus cDNA clone IMAGE:446076 5' similar to
TR:O08722 O08722 TRANSMEMBRANE RECEPTOR ***UNC5H2***
. ;, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 94 a 157 c 147 g 119 t

COMMENT:

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Possible reversed clone: similarity on wrong strand
MGI:271412
Seq primer: -40RP from Gibco
High quality sequence stop: 478
POLYA=No.

REFERENCE: 1 (bases 1 to 517)
AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;
Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.;
Allen,M.; Bowers,Y.; Person,B. ; Swaller,T.;
Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E. ;
Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;
Waterston,R.; Wilson,R.
TITLE (TI): The WashU-NCI Mouse EST Project 1999
JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..517	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="IMAGE:446076" /clone-lib="Soares mouse placenta 4NbMP13.5 14.5" /sex="unknown" /tissue-type="placenta" /dev-stage="adult" /lab-host="DH10B" /note="Organ: placenta; Vector:

modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAA TTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

SEQUENCE (SEQ):

```

1  gtgaccactc  tgcccagctg  gaccagcctc  cattcacatt  tatgatgact  gtggccgtgg
61  tgctccggcg  cttggccact  atattcttgg  ccacacaggt  gtagttggcc  gtgtctgaga
121  ggcgcgcctg  gcggatgatg  aggttggtgg  caatggtgag  caggaagtta  gtgtcctgag
181  cggggtcaat  gacatcttca  ttcttgagcc  attccacctc  agccacaggc  actccctccg
241  gtgggcggca  ctgcagaagg  acctcatgat  ccaagggtag  ctccttggcc  agaggctcct
301  ggtcaaagtt  cttgcgcaag  taggcaatgc  ggatgtaggc  tcggcgactc  ttggtagttc
361  ccgaagagct  ccaggccacg  cactggcacc  agtagtcctc  gagcccgaag  agttcctcca
421  cttgctgccc  tgacacctcg  atctgcacct  ctgcaccccg  caagcctgtg  gcctcatcca
481  ggctctcctg  tgtgacgtgg  tcattctggc  tgacca

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L2 ANSWER 304 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): AI430657 GenBank (R)
 GenBank ACC. NO. (GBN): AI430657
 GenBank VERSION (VER): AI430657.1 GI:4276493
 CAS REGISTRY NO. (RN): 226599-12-8
 SEQUENCE LENGTH (SQL): 645
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 15 Mar 2000
 DEFINITION (DEF): mc52e07.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:352164 5' similar to TR:008722 008722 TRANSMEMBRANE RECEPTOR ***UNC5H2***
 . ; , mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 131 a 209 c 176 g 129 t

COMMENT:

Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the correct orientation)
 MGI:223964
 Seq primer: -40RP from Gibco
 High quality sequence stop: 467
 POLYA=No.

REFERENCE: 1 (bases 1 to 645)
 AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.; Allen,M.; Bowers,Y.; Person,B. ; Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E. ;

TITLE (TI):
JOURNAL (SO):

Waterston, R.; Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..645	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="IMAGE:352164" /clone-lib="Soares mouse embryo NbME13.5 14.5" /sex="unknown" /tissue-type="embryo" /dev-stage="13.5-14.5dpc total fetus" /lab-host="DH10B" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAA TTTTTTTTTTTTTTTTTTTTTTTTTTT T 3'] , on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2] ; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "

SEQUENCE (SEQ):

```
1  gtccatggac  cggtacctaa  actacttcgc  caccaaagct  agtccacacag  gtgtcatctt
61  agacctctgg  gaagctcggc  aacaggatga  cggggacctc  aacagcctgg  ccagtgcctt
121  ggaggagatg  ggcaagagtg  agatgctggt  agccatggcc  acagatggcg  attgctgagt
181  gcctgtgacc  acaggctgtg  gggatcagta  ggagacggtg  caaggaggcc  tggcagcctc
241  tgcacagggg  tgcccagcct  ccaccactcc  tggctcacag  caggaatggt  ccttcaactc
301  cctccccgcc  acaaccctca  gaccaccacc  accagcctta  gaaagtctct  gtgctctact
361  ggcaaagagg  ccgggatcct  ctggcccact  gtttccccag  ctactctctg  ggtgggctga
421  ggctctctgg  acagctgaaa  gccagaggct  ttcctctgcg  acaacacacc  accctcagcc
481  ctgtgacttt  ggggaccac  aggtttcaat  ttctgtgtca  catggtctct  ggctagggac
541  cgctctctta  tccctggatc  tttcagggct  ctctggtccc  ccattcttag  gctcccaggc
601  atccgagaca  gcaccttcct  cccaccctca  gaggtcaagt  ggggt
```

L2 ANSWER 305 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): CEU62639 GenBank (R)
GenBank ACC. NO. (GBN): U62639
GenBank VERSION (VER): U62639.1 GI:4097486
CAS REGISTRY NO. (RN): 224328-12-5
SEQUENCE LENGTH (SQL): 3935
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Invertebrates
DATE (DATE): 26 Jan 1999
DEFINITION (DEF): Caenorhabditis elegans lipoprotein receptor precursor
(lr) gene, complete cds.
SOURCE: Caenorhabditis elegans.
ORGANISM (ORGN): Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

NUCLEIC ACID COUNT (NA): 1100 a 830 c 841 g 1164 t
REFERENCE: 1 (bases 1 to 3935)
AUTHOR (AU): Tang, P.; Kingston, I.B.
TITLE (TI): Genomic organization of the *Caenorhabditis elegans* lipoprotein receptor (lr) gene
JOURNAL (SO): Unpublished
REFERENCE: 2 (bases 1 to 3935)
AUTHOR (AU): Tang, P.; Kingston, I.B.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (01-JUL-1996) Department of Parasitology, Chang Gung College of Medicine and Technology, 259 Wen-hwa 1st Road, Kweishan, Taoyuan 333, Taiwan

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..3935	/organism="Caenorhabditis elegans" /strain="Bristol N2" /db-xref="taxon:6239" /chromosome="IV" /map="between unc5 and rtw7" /clone="#CB1007" /note="see GenBank Accession Number U62281 for cDNA"
gene	203..3934	/gene="lr"
CAAT-signal	203..207	/gene="lr"
CAAT-signal	616..620	/gene="lr"
sig-peptide	join(841..897,946..966)	/note="inverted" /gene="lr"
mRNA	join(<841..897, 946..1497,1544..2393, 2439..2629,2680..2888, 2933..3934)	/gene="lr"
CDS	join(841..897, 946..1497,1544..2393, 2439..2629,2680..2888, 2933..3851)	/gene="lr" /note="similar to low density lipoprotein receptor" /codon-start=1 /protein-id="AAD09364.1" /db-xref="GI:4097487" /translation="MRTMRLAWLLPLFIHILIKN TAQAPAVNNSTCDQAKEFDCGNGR LRCIPAEWQCDNVADCDKGRDESGCSYAAHHCSTS FMLCKNGLCVANEFKCDGEDDCRD GSDEQHCEYNILKSRFDGSNPSAPTTFVGHNGPE CHPPRLRCRSGQCIQPDLCVCDGHQ DCSGGDDEVNCTRRGHENMQSSTDFFHDDVHLVDP TFFANEDNKRSGYTMCHSGDVC PDSFLCDGDLDCDDASDEKNCQTNAPSEEEYLSG QADHMHSCSAAGMYSCGTKGSEIG VCIPMNATCNGIKECPLGDDESKHCSECARKRCD HTCMNTPHGARCICQEGYKLADDG LTCEDEDECATHGHLCCQHFCEDRLGSFACKCANG YELETDGHSCKYEATTTPEGYLFI SLGGEVRQMPLADFTDGSNYSIAIQKFAGHGTIRS IDFMHRNNKMFMSISDEHGDPTGE LSVSDNGLMRVLRENVIGVSNVAVDWIGGNVFFT QKSPSPSAGISICTMSGMFCRRVI EGKEQQQSYRGLVVHMPMRGLIIWIDSYQKYHRIM MANMDGSQVRILLDNKLEVP SALA IDYIRHDVYFGDVERQLIERVNIDTKERRVVISN GVHHPYDMAYFNGFLYWADWGSES LKVQEMTHHHSSPQVIHTFNRYPYGIAVNHSLYQ TGPPSNPCLELECPWLCVIVPKSD FIMTAKVCPCDGYTHSVTENS CIPVPTIEDEENL EKLSHIGSALMAEYCEAGVACMNG

		EKFSAMEEDSSLWLIVLLLI FLI IVAVVGIIAFLWFSQQEHMKDVISTARVRVDNMA RKAEDAAPIVEKFRKVTDKQRST PPREGCQTATNVDFVSYETNAEKRIRMDSSPTS GNPMYDEVPESSSTGFVRSASAPFA GVIRFENDSLL"
misc-feature	join(967..1497, 1544..1837)	/gene="lr"
		/note="encodes ligand binding domain"
misc-feature	967..1095	/gene="lr"
		/note="encodes class A ligand binding repeat"
mat-peptide	join(967..1497, 1544..2393,2439..2629, 2680..2888,2933..3848)	/gene="lr"
		/product="lipoprotein receptor"
misc-feature	1096..1215	/gene="lr"
		/note="encodes class A ligand binding repeat"
misc-feature	1285..1401	/gene="lr"
		/note="encodes class A ligand binding repeat"
misc-feature	join(1483..1497, 1544..1651)	/gene="lr"
		/note="encodes class A ligand binding repeat"
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LOCUS (LOC): AI334729 GenBank (R)
 GenBank ACC. NO. (GBN): AI334729
 GenBank VERSION (VER): AI334729.1 GI:4071656
 CAS REGISTRY NO. (RN): 224003-40-1
 SEQUENCE LENGTH (SQL): 313
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 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 15 Feb 1999
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 IMAGE:1998403 3' similar to TR:008721 008721
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 SOURCE: human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 62 a 107 c 89 g 55 t
 COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 934 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 309.

REFERENCE: 1 (bases 1 to 313)
 AUTHOR (AU): NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute / National Institute of
 Neurological Disorders and Stroke, Brain Tumor Genome
 Anatomy Project (CGAP/BTGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1998)

FEATURES (FEAT):

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 CAS REGISTRY NO. (RN): 208428-65-3
 SEQUENCE LENGTH (SQL): 264
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 27 May 1998
 DEFINITION (DEF): am80d11.s1 Stratagene schizo brain S11 Homo sapiens
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 TRANSMEMBRANE RECEPTOR ***UNC5H1*** . ;, mRNA
 sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 52 a 64 c 91 g 57 t
 COMMENT:
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: polyT not found
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 162.
 REFERENCE: 1 (bases 1 to 264)
 AUTHOR (AU): Hillier,L.; Allen,M.; Bowles,L.; Dubuque,T.; Geisel,G.;
 Jost,S.; Krizman,D.; Kucaba,T.; Lacy,M.; Le,N.;
 Lennon,G.; Marra,M.; Martin,J. ; Moore,B.;
 Schellenberg,K.; Steptoe,M.; Tan,F.; Theising,B.;
 White,Y.; Wylie,T.; Waterston,R.; Wilson,R.
 TITLE (TI): WashU-NCI human EST Project
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..264	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1629429" /clone-lib="Stratagene schizo brain S11" /sex="male" /tissue-type="schizophrenic brain S-11 frontal lobe" /dev-stage="34 years old" /lab-host="SOLR (kanamycin resistant)" /note="Vector: Bluescript SK-; Site-1: EcoRI; Library constructed from S-11 frontal lobe, male, 34 years old, 50% caucasian, 50% Aleutian. Schizophrenic suicide. Random primed into EcoRI site of ZAP II Vector. Mass excised. Custom library. Avg insert length 1.4kb. Material obtained by Johnston N., Torrey, E.F., Yolken R., and the Stanley Neuropathology Consortium - Analysis of RNAs from the Brains

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L2 ANSWER 308 OF 313 GENBANK.RTM. COPYRIGHT 2005 on STN

LOCUS (LOC): RNU87306 GenBank (R)
GenBank ACC. NO. (GBN): U87306
GenBank VERSION (VER): U87306.1 GI:2055393
CAS REGISTRY NO. (RN): 391843-13-3
SEQUENCE LENGTH (SQL): 2838
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Rodents
DATE (DATE): 15 May 1997
DEFINITION (DEF): Rattus norvegicus transmembrane receptor ***Unc5H2***
mRNA, complete cds.
SOURCE: Norway rat.
ORGANISM (ORGN): Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus
NUCLEIC ACID COUNT (NA): 588 a 892 c 804 g 553 t 1 others
REFERENCE: 1 (bases 1 to 2838)
AUTHOR (AU): Leonardo,E.D.; Hinck,L.; Masu,M.; Keino-Masu,K.;
Ackerman,S.L.; Tessier-Lavigne,M.
TITLE (TI): Vertebrate homologues of C. elegans UNC-5 are candidate
netrin receptors
JOURNAL (SO): Nature, 386 (6627), 833-838 (1997)
OTHER SOURCE (OS): CA 127:15863
REFERENCE: 2 (bases 1 to 2838)
AUTHOR (AU): Leonardo,E.D.; Hinck,L.; Masu,M.; Keino-Masu,K.;
Tessier-Lavigne,M.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus,
San Francisco, CA 94143-0452, USA

FEATURES (FEAT):

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2641	cggctgttgg	cacagaagct	ctccatggac	cggtagctga	actacttcgc	caccaagct
2701	agtcccacag	gcgtgatctt	agacctctgg	gaagctcgcc	agcaggatga	tggggacctc
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LOCUS (LOC): RNU87305 GenBank (R)
 GenBank ACC. NO. (GBN): U87305
 GenBank VERSION (VER): U87305.1 GI:2055391
 CAS REGISTRY NO. (RN): 384753-38-2
 SEQUENCE LENGTH (SQL): 2697
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 15 May 1997
 DEFINITION (DEF): Rattus norvegicus transmembrane receptor ***Unc5H1***
 mRNA, complete cds.
 SOURCE: Norway rat.
 ORGANISM (ORGN): Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Rattus
 NUCLEIC ACID COUNT (NA): 541 a 864 c 766 g 526 t
 REFERENCE: 1 (bases 1 to 2697)
 AUTHOR (AU): Leonardo,E.D.; Hinck,L.; Masu,M.; Keino-Masu,K.;
 Ackerman,S.L.; Tessier-Lavigne,M.
 TITLE (TI): Vertebrate homologues of C. elegans UNC-5 are candidate
 netrin receptors
 JOURNAL (SO): Nature, 386 (6627), 833-838 (1997)
 OTHER SOURCE (OS): CA 127:15863
 REFERENCE: 2 (bases 1 to 2697)
 AUTHOR (AU): Leonardo,E.D.; Hinck,L.; Masu,M.; Keino-Masu,K.;
 Tessier-Lavigne,M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus,
 San Francisco, CA 94143-0452, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
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CDS	1..2697	/codon-start=1 /product="transmembrane receptor UNC5H1" /protein-id="AAB57678.1" /db-xref="GI:2055392" /translation="MAVRPGLWPVLLGIVLA AWL RGSGAQQSATVANPVPGANPDLLP HFLVEPEDVYIVKNKPVLLVCKAVPATQIF FKCN GEWVRQVDHVIERSTDSSSGLPTM EVRINVSROQVEKVFGLLEEWCVQCVAWSS SGTTK SQKAYIRIAYLRKNFEQEPLAKEV SLEQGIVLPCRPPGIPPAEVEWLRNEDLVD PSL DPNVYITREHSLVVRQARLADTAN YTCVAKNIVARRRSTSAAVIVYVNGGWSTW TEWS VCSASCGRGWQKRSRSTNPAPLN GGAFCEGQNVQKTACATLCPVDGSWSSWSK WSAC GLDCTHWSRECSDPAPRNGGEEC RGADLDTRNCTSDLCLHTASCPEDVALYIGL VAV AVCLFLLLLALGLIYCRKKEGLDS DVADSSILTSGFQPVSIKPSKADNPHLLTIQ PDL STTTTTYQGSLSRQDGPSPKFQL SNGHLLSPLGSGRHTLHHSSPTSEAEDFVS RSLST QNYFRSLPRGTSNMAYGTFNFLGG RLMIPNTGISLLIPPDAIPRGKIYEIYLT LHKPE DVRLPLAGCQTLLSPVVS CGPPGV LLTRPVILAMDHCGEPSPDWSLRLKKQSC EGSW EDVLHLGEESPSHLYYCQLEAGAC

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 QLEKQLGGQLIQEPRVLHFKDSYHNLRLSIHDVP
 SSLWKSLLVSYQEIPFYHIWNGT
 QQYLHCTFTLERINASTSDLACKVWVWQVEGDGQ
 SFNINFNITKDTRFAELLALESEG
 GVPALVGPSAFKIPFLIRQKIIASLDPPCSRGA
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 FTVSEAEAC"

SEQUENCE (SEQ) :

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121	gacctgctgc	cccacttcct	ggtagagcct	gaggacgtgt	acattgtcaa	gaacaagccg
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1321	caggatggac	ccagccccc	gttccagctc	tctaattggtc	acctgctcag	cccactgggg
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1441	cgcccttcca	cccaaaacta	ctttcgttcc	ctgccccgcg	gcaccagcaa	catggcctac
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1561	atacccccg	atgccatccc	ccgaggaaag	atctacgaga	tctacctcac	actgcacaag
1621	ccagaagacg	tgagggttgc	cctagctggc	tgctcagacc	tgctgagtcc	agtcgttagc
1681	tgtggggccc	caggagtctt	gctcaccgcg	ccagtcaccc	ttgcaatgga	ccactgtgga
1741	gagcccagcc	ctgacagctg	gagtctgcgc	ctcaaaaagc	agtcctgcga	gggcagttgg
1801	gaggatgtgc	tgacaccttg	tgaggagtca	ccttcccacc	tctactactg	ccagctggag
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L2 ANSWER 310 OF 313 CONFSCI COPYRIGHT 2005 CSA on STN
 AN 2004:74237 CONFSCI
 DN 04-074237
 TI Differential co-involvement of Babo/dSmad2-mediated TGF- β signaling and
 netrin/Frazzled/ ***UNC5*** in guidance of axons versus dendrites
 AU Zheng, X.
 SO Cold Spring Harbor Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring
 Harbor, NY 11724-2213, USA; phone: 516-367-8346; fax: 516-367-8845; email:
 meetings@cshl.edu; URL: meetings.cshl.edu.
 Meeting Info.: 000 7536: Axon Guidance & Neural Plasticity (0007536). Cold
 Spring Harbor, NY (USA). 18-22 Sep 2004. Cold Spring Harbor Laboratory.

FS DCCP
LA English

L2 ANSWER 311 OF 313 CONFSCI COPYRIGHT 2005 CSA on STN
AN 2004:74121 CONFSCI
DN 04-074121
TI Control of glial position via the repulsive netrin receptor ***UNC5***
AU McKinnon, R.D.
SO Cold Spring Harbor Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring Harbor, NY 11724-2213, USA; phone: 516-367-8346; fax: 516-367-8845; email: meetings@cshl.edu; URL: meetings.cshl.edu.
Meeting Info.: 000 7536: Axon Guidance & Neural Plasticity (0007536). Cold Spring Harbor, NY (USA). 18-22 Sep 2004. Cold Spring Harbor Laboratory.

DT Conference
FS DCCP
LA English

L2 ANSWER 312 OF 313 CONFSCI COPYRIGHT 2005 CSA on STN
AN 2004:74086 CONFSCI
DN 04-074086
TI Fra-dependent and Fra-independent ***UNC5*** repulsion controls differential dorsoventral positioning of motoraxons through enabled
AU Labrador, J.
SO Cold Spring Harbor Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring Harbor, NY 11724-2213, USA; phone: 516-367-8346; fax: 516-367-8845; email: meetings@cshl.edu; URL: meetings.cshl.edu.
Meeting Info.: 000 7536: Axon Guidance & Neural Plasticity (0007536). Cold Spring Harbor, NY (USA). 18-22 Sep 2004. Cold Spring Harbor Laboratory.

DT Conference
FS DCCP
LA English

L2 ANSWER 313 OF 313 CONFSCI COPYRIGHT 2005 CSA on STN
AN 2004:74047 CONFSCI
DN 04-074047
TI Suppression of Frazzled dependent netrin relocation by ***UNC5***
AU Hiramoto, M.
SO Cold Spring Harbor Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring Harbor, NY 11724-2213, USA; phone: 516-367-8346; fax: 516-367-8845; email: meetings@cshl.edu; URL: meetings.cshl.edu.
Meeting Info.: 000 7536: Axon Guidance & Neural Plasticity (0007536). Cold Spring Harbor, NY (USA). 18-22 Sep 2004. Cold Spring Harbor Laboratory.

DT Conference
FS DCCP
LA English

STN INTERNATIONAL LOGOFF AT 11:14:42 ON 15 MAR 2005